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Enhancing the breed analysis of the Dohne Merino by accounting for heterogeneous variances and phantom parents

by
Wilmari Jordaan

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Supervisor: Prof SWP Cloete
Co-supervisors: Prof K Dzama
Dr JJ Olivier

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Abstract

Genetic (co)variances for body weight, clean fleece weight and fibre diameter were estimated for the South African Dohne Merino using data transformed as proportions of contemporary group means. The data analysed included body weight, clean fleece weight and fibre diameter records for 282 513 animals, evaluated between 1992 and 2011. There were 5 698 sires, 105 886 dams and 6 291 contemporary groups in the data. A three-trait animal model was fitted, where the random variables were the direct additive genetic effects, as well as the sire-flock-season (SFS) interaction, while the fixed effects included contemporary groups (FYSSM) (6 291 classes), birth status (single, twins or triplets), age of dam (1 to 3 years), which was plotted as a linear regression as well as age at performance measurement, which was fitted as a polynomial.

The direct heritability estimates (SE) for body weight, clean fleece weight and fibre diameter were 0.265 (0.005), 0.210 (0.004) and 0.437 (0.005), respectively. Genetic correlations for body weight with clean fleece weight and fibre diameter were 0.035 (0.015) and 0.139 (0.011), respectively, while the genetic correlation between clean fleece weight and fibre diameter was 0.169 (0.012). Body weight had phenotypic correlations of 0.327 (0.002) and 0.150 (0.002), respectively, with clean fleece weight and fibre diameter, which had a phenotypic correlation of 0.190 (0.002) with clean fleece weight. The moderate to high heritability estimates suggests that there is substantial genetic variation, which may result in genetic improvement if selection is applied on these traits. Genetic correlations were generally low, suggesting that progress in all these traits was possible in a scientific selection program. Genetic trends derived during the study supported the contention that genetic progress in all traits was attainable in a well-constructed breeding programme.

Transformation of the data to percentages of contemporary groups resulted in adjustments to breeding values. The breeding values for sires originating from flocks maintained in limiting environments (Low group; 180 sires) were adjusted upwards, while those of sires originating from a non-limiting production environment (High group; 146 sires) were adjusted downwards. These effects were markedly obvious for the quantitative traits (body weight and clean fleece weight), but to a much lesser extent for fibre diameter. This transformation resulted in the genetic trends for the Low groups being adjusted to be comparable to those in the High group for body weight and Fibre diameter. It was concluded that sire breeding values derived from transformed data would be more robust across the typical diverse environments supporting local Dohne Merino production.

The genetic value of animals entering the recorded population from a commercial base (F4 animals) was below the fully recorded part of the population. The inclusion of phantom parent groups in the genetic analysis rendered genetic trends in F4 animals comparable to that of the pedigreed portion of animals in the analyses. It was concluded that animals from a commercial base (which are alleged to have advantages in terms of fitness and robustness) were more likely to perform satisfactorily for selection with the inclusion of phantom groups than without it.

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It was recommended that data in the national Dohne Merino analysis be transformed proportion of contemporary group means to account for heterogeneous contemporary group variances. Phantom parent groups should also be applied to the analysis to increase the probability of those animals entering the breeding flock from a commercial base being selected.

Keywords: Dohne Merino, heterogeneous variance, phantom groups

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Samevatting

Genetiese kovariansies vir liggaamgewig, skoonvaggewig en veseldikte is vir die SA Dohne Merino bevolking in Suid-Afrika beraam nadat data getransformeer as ‘n proporsie van die kontemporêre groep gemiddelddes uitgedruk is. Die data het rekords in van liggaamsgewig, skoonvaggewig en veseldikte van 282 513 diere oor die tydperk van 1992 tot 2011 ingesluit. Die data sluit rekords van 5 698 vaars, 105 886 moers en 6 291 kontemporêre groepe in. 'n Meer-eienskapdieremodel met 'n additiewe diere-effekte sowel as 'n vaar-kudde-seisoen (SFS) interaksie is as ewekansige effekte gemodelleer, bykomstig tot die vaste effekte van kontemporêre groep (FYSSM) (6 291 klasse), geboortestatus (enkelling, tweeling of drieling), ouderdom van moer (1 tot 3 jaar) gepas as 'n lineêre regressive, sowel as ouderdom by prestasie meting as ‘n polinoom gepas.

Die beraamde direkte oorerflikheid (SF) van liggaamgewig, skoonvaggewig en veseldikte van die meereienskap dieremodel was onderskeidelik 0,265 (0,005), 0,210 (0,004) en 0,437 (0,005). Die genetiese korrelasies van liggaamsgewig met skoonvaggewig en veseldikte was 0,035 (0.015) en 0,139 (0.011) onderskeidelik, terwyl die genetiese korrelasie tussen skoonvaggewig en veseldikte 0,169 (0.012) beloop het. Liggaamsgewig het onderskeie fenotipiese korrelasies van 0,327 (0.002) en 0.150 (0.002) met skoonvaggewig en veseldikte gehad, terwyl skoonvaggewig ‘n fenotipiese korrelasie van 0.190 (0.002) met veseldikte gehad het. Die medium tot hoë oorerflikheidhede dui daarop dat daar aansienlike genetiese variasie voorkom, wat kan aanleiding gee tot genetiese vordering as seleksie op die eienskappe toegepas word. Genetiese korrelasies was oor die algemeen laag wat daarop dui dat vordering in al die eienskappe deur ‘n wetenskaplike seleksie program moontlik is. Die aanspraak is deur genetiese tendense in die studie bevestig.

Die transformasie van data na proporsies van kontemporêre groep gemiddeldes het daartoe gelei dat teelwaardes aangepas word. Die teelwaardes van vaars uit kuddes met ‘n omgewing wat beperk word (Lae groep:180 vaars), is opwaarts aangepas. Daarenteen is vaars uit 'n nie-beperkende produksie omgewing (Hoë groep:146 vaars) se teelwaardes afwaarts aangepas. Hierdie effekte was veral ooglopend vir die kwantitatiewe eienskappe, liggaamgewig en skoonvaggewig, maar tot 'n mindere mate vir veseldikte. Die transformasie het daartoe gelei dat die genetiese tendense for die Lae groep aangepas word om vergelykbaar te wees met die Hoë groep vir liggaamsgewig en skoonvaggewig. Die gevolgtrekking was gemaak dat meer toepaslike vaar teelwaardes, bereken vanaf getransformeerde data, verkry word vir regoor die diverse omgewings wat produksie van plaaslike Dohne Merinos ondersteun.

Die genetiese waarde van diere wat die aangetekende populasie uit ‘n kommersiële agtergrond (F4 diere) binnekom was laer as die volledig aangetekende gedeelte van die populasie. Die insluiting van skimgroepe in die genetiese ontleding het tot genetiese tendense gelei wat die F4 diere vergelykbaar gemaak het met diere in die ontleding wat wel stamboekinligting het. Die gevolgtrekking is gemaak dat diere van ‘n

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kommersiële agtergrond (wat aanvaar word om voordele in te hou in terme van fiksheid en robuustheid) meer geredelik geselekteer sal word vir die stoet met die insluiting van skimgroepe as daarsonder.

Dit word aanbeveel dat die data in die Nasionale Dohne Merino na proporsies van die kontemporêre groepgemiddeldes getrensformeer word om vir heterogene kontemporêre groep variansies voorsiening te maak. Skimgroepe moet ook gepas word in die ontleding om die waarskynlikheid te verhoog dat diere vanuit 'n kommersiële basis, ook geselekteer sal word.

Kern woorde: Dohne Merino, heterogene variansies, skimgroepe

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Chapter 1

General introduction

The Dohne Merino is a synthetic, dual-purpose sheep breed, thus emphasizing both wool and meat (mutton and lamb) production. The breed originated from a cross between the German Mutton Merino ram(s) and South African Merino ewe(s) (Kotze, 1951) and through a interbreeding and a selection program with this initial cross the Dohne Merino was developed (McMaster 2005a). Swanepoel (2006) did a comprehensive study on the Dohne Merino in which the history of the breed was discussed comprehensively. The establishment of the breed was prompted by the need for a wool breed adapting well to semi-intensive farming conditions prevalent in the Eastern Cape grassland regions (Cloete *et al*., 1998). According to the latter authors, the breed has since also spread to other parts of South Africa, including the Western Cape. In later years it has indeed become an international breed, with active breeder's societies in Australia (138 according to McMaster 2005b) and elsewhere.

Pertaining to the national Dohne Merino population, it is noteworthy that sufficient links exist between individual flocks resulting from a general exchange of breeding material in the stud industry by making use of the sire-referencing scheme (Swanepoel, 2006). The breed structure and the availability of production records linked to contemporary groups pedigree information culminated in a breed analysis of the national flock by 2008 (Van Wyk *et al*., 2008).

According to Delport *et al.* (2003), the Dohne Merino Breed Society has developed structures to enhance the genetic progress of the breed by changing genetic evaluations from within-flock to across flocks. Data used for the genetic evaluation of the Dohne Merino breed originate from a vast array of environments in South Africa, with 9 biomes and 5 different aridity classes (Palmer and Ainslie, 2006). This level of diversity results in marked differences in production levels (a whole range from marginal to high and intensive production areas and systems) as well as contemporary group means. This structure will lead to implications in the variance, within the contemporary groups, resulting in scale effects on the estimated breeding values. Without adjustment, animals within contemporary groups of higher mean will also have greater variance, which might lead to increased variation in the estimated breeding values of such animals. Also, estimated breeding values may not predict progeny performance reliably across different production environments. The expression of traits as proportions of their contemporary group means is one method that can be used to rectify this situation. Brown *et al*. (2005) found that data transformed accordingly to proportions of their contemporary group means resulted in slightly higher heritability estimates, while the resultant estimated breeding values also reflected the phenotypic differences better in different production environments.

Registered Dohne Merino breeders make use of an open nucleus system, which is part of the upgrading system advocated by the Breeder's Society. This allows a two-directional flow of genetic material, where the top ewes in commercial flocks always move to the stud and top rams bred in the stud are used in the

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commercial flock. Mueller and James (1984) stated that there is increased additive genetic variation resulting from genetic differences between levels in this system; hence the expected genetic gain is increased relative to equivalent single flocks, provided more females than males need to be replaced. Ewes resulting from a cross between F2 ewes and Dohne Merino stud rams are used because only a maximum of 20% of the flock ewes may be moved to stud, if approved according to the Dohne Merino Breeder's Society standards. With this strict selection (selecting fewer ewes but of higher quality), this may lead to an acceleration of genetic progress (Dohne Merino Handleiding, 2009). However, the animals (F3's) entering the stud flock lack pedigree information of at least one parent, causing a deviation in their genetic level as well as selection intensity bestowed on such animal (Theron *et al*., 2002; Schaeffer 2006). Breeding values for such animals would therefore not being estimated accurately. Schaeffer (2006) suggested that the unknown parent could be assigned to a phantom group corresponding to the year of birth of the animal and to the sex of the parent as well as sex of the offspring of which there are four possible pathways of selection (each pathway has different selection intensity). Theron *et al*. (2002) has demonstrated that linking these animals to phantom parent groups reduces bias in the estimation of genetic trends.

Considerable evidence for tangible progress in fleece traits, and in a range of meat production traits as well as for adaptation traits has been reported in the Australian sheep and wool industries (Banks and Brown, 2009). According to Adams and Cronje (2003), there is an increased economic pressure on the Merino industry to produce finer wool while also producing more meat. According to genetic parameters for woolled sheep reviewed by Safari *et al*. (2005) this is not a straightforward objective as there are several unfavourable genetic correlations among key traits. Banks and Brown (2009) therefore suggested that the Merino population is evolving towards two broad types – one that focuses on high quality (fine) wool and the other a more dual purpose animal. By exploiting the available genetic diversity of the sheep we can rapidly increase profitability.

1.1 The objectives of the study

As a point of departure, it is clear that data used for the genetic evaluation of the Dohne Merino population maintained by the Dohne Merino Breeder's Society in South Africa originates from a wide range of environments. In these environments, there are marked differences in production levels and contemporary group means. Heterogeneous genetic variances across groups can therefore occur when genetic differences are expressed more in superior environments when compared to inferior environmental conditions (Brown *et al*., 2005). These differences are likely to affect the estimated breeding values (EBV's) if the within contemporary group means of the data are not accounted for in a proper manner by linking the flocks at all levels of the industry. Brown *et al*. (2005) stated that animals from groups with higher means are likely to have greater variation in the EBVs if not adjusted for properly, leading to the EBVs not predicting progeny performance reliably across the different production environments.

Furthermore, animals entering the breeding flock from a commercial base (F3 animals) lack pedigree information and all these animals are reverted back to the base population, which will cause their derived

breeding values to be underestimated. This will lead to the progeny of such animals being less likely to be selected. As a result, the advantages sought for, in terms of robustness and fitness, may not be realised. Animals entering the recorded population may alternatively be allocated to specified groups according to the information that is available for each of them. Groups constructed in this way during genetic evaluation are commonly referred to as phantom groups (Theron *et al*., 2002; Fikse, 2009). By allocating the base animals to phantom groups it is possible to exert some control over the genetic levels that they may represent in the broader population (Westall *et al*., 1988).

Therefore the aim of this study was to determine:

- the effect of transforming data to account for the heterogeneity of contemporary group variances on the accuracy of breeding values under different conditions and genetic trends
- the effect of phantom group classification for animals entering the National Dohne Merino breeding flock from the commercial industry on the breeding values of such animals as well as the genetic trends derived from the analysis.

The effect of transforming national Dohne Merino data to adjust for heterogeneous contemporary group means and the implementation of phantom groups to adjust for differences among base animals on national breeding values were thus considered for three key production and wool quality traits, namely; bodyweight, clean fleece weight and fibre diameter.

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Chapter 2

Literature review

2.1 Background

The Dohne Merino is a synthetic dual-purpose sheep breed, thus emphasizing both wool and meat (mutton and lamb) production. When looking at the history of the Dohne Merino the breed originated from a cross between German Mutton Merino ram(s) and South African Merino ewe(s) (Kotze, 1951).

The breeding program was initiated in 1939 and the progeny was interbred and visually selected for Merino-type wool and rapid growth rate in lambs under commercial rangeland conditions. High mortality rates and low fertility limited the production of Merino sheep in the Eastern Cape sour grassveld region at that stage. During that period Merino sheep had excessive skin folds that resulted in high levels of wool production but also in the animals being susceptible to fleece rot and blowfly strike. Due to the selective grazing habits of the Merino a higher input cost was furthermore incurred. A more intensive management strategy was therefore needed to maintain a sustainable woolled sheep enterprise. Due to the fact that profitability was compromised, farmers decided upon a more extensive farming system that would involve a more adaptable bloodline. The primary driver of a profitable enterprise is a higher generated income from wool and mutton. An increase in reproduction rate, improved marketability of slaughter lambs and surplus breeding material contribute to this objective. The Dohne Merino was developed to fulfil this need.

The development of the Dohne Merino, as initiated and implemented by Mr. J.J.J. Kotze, was always closely related to the Dohne Agricultural Research Station situated in the Eastern Cape (27°28’ longitude; 32°32’ S latitude) according to McMaster (1991) as cited by Swanepoel (2006) hence the name of the breed Dohne Merino. This Research station is situated at an altitude of 1020m above sea level 72km from the coast in a summer rainfall area with an average annual precipitation of 598mm (Stutterheim climate, 2000) within a mist belt, and is characterized by particularly dry winters and wet and humid summers. The locality is characterized by a severe challenge of internal parasites as well as blowflies, to name but a few of the challenges in this region for sheep breeders. Registered Dohne Merino breeders are situated in a vast array of environments in South Africa, with 9 biomes and 5 different aridity classes (Palmer and Ainslie, 2006), ranging from semi-intensive and intensive operation under favourable climatic conditions to very extensive farming operations in arid regions with a low carrying capacity.

The Dohne Merino Breeder’s Society was formed in 1966. Selection was based on performance testing since 1974. In *circa* 1985 a computerized flock-recording scheme was introduced (GJ Delport, personal communication) where raw on-farm data was collected by breeders, which included quantitative and

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qualitative wool traits, as well as live bodyweight data (Swanepoel, 2006). The Breeder's Society is responsible for the handling of the weaning weights as well as birth registration and also oversees the final selection and registration of breeding material. Since the 1990's the Society calculated BLUP estimated breeding values (EBV's) for registered breeders but only on a within-flock basis. The grading of animals was still performed on a within-flock basis, mainly due to the fact that the breeders relied on an index system managed by the Society. According to Delport *et al.* (2003) the Dohne Merino Breeder's Society was at that stage developing structures to enhance the genetic progress of the breed by changing the genetic evaluations from within-flock to across flock evaluations. This being affected for a decade, sufficient links now exist between flocks as a result of the general exchange of breeding material in the Dohne Merino stud industry. This was, among others, achieved by making use of a sire-referencing scheme (Swanepoel, 2006). Across-flock breeding values were therefore already available after the Swanepoel (2006) analysis and the process of moving from within flock to across-flock evaluations is presently being refined. This culminated in a breed analysis of the national flock by 2008 (Van Wyk *et al*., 2008).

Recently, in Australia, there is considerable evidence for increasingly rapid progress, both in fleece traits and in a range of meat production traits as well as for adaptation traits (Banks and Brown, 2009). Banks and Brown (2009) suggests that the broader Australian Merino population is evolving towards two broad types – one that focuses on high quality wool that is finer than 19 micron with a wool/meat income ratio of about 3:1, and the other towards a more dual-purpose animal that produces medium wool of 19-21 µm and maintains a wool/meat income ratio between 1.5:1 and 1:1. By exploiting the available genetic diversity of the ovine genetic resource to our disposal, we can rapidly increase profitability. Olivier *et al*. (2010) stated that wool income from a dual-purpose breed could possibly be doubled by reducing fibre diameter from 22 µm to 18 µm if all other production traits were maintained. This was achieved in the Grootfontein Dohne Merino flock but the latter authors also found that further selection for a reduced fibre diameter would be complicated by the high occurrence of creeping belly and by an increase in the production of wool with a low staple strength.

From this discussion it is evident that the Dohne Merino is a dynamic breed that plays an important role in the South African small stock industry. According to Cloete and Olivier (2010) approximately a quarter of weaning weights submitted to the National Small Stock Improvement Scheme (NSSIS) database came from Dohne breeders. It is thus evident that the breed enjoys a considerable support base in the local small stock industry. Yet there are a number of issues that needs to be addressed to ensure that the breed stays on the forefront of genetic evaluation. These issues include properly accounting for heterogeneous contemporary group variances, as well as for the upgrading of animals in the breed from a commercial, unrecorded base. These issues will now be discussed.

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2.2 Heterogenous variances

2.2.1 Understanding heterogeneity

In the past researchers whom studied psychology viewed heterogeneity of variance as a methodological nuisance and as an unwelcome obstacle in the pursuit of inferences about the effects the experimental treatments had on the means. Heterogeneity is likely to occur in program evaluation studies (Light and Smith, 1971). Bryk and Raudenbush (1988) showed that the presence of heterogeneity of variance across groups in experiments indicates that treatments have differential effects across individuals (subjects). The latter authors also suggested that, rather than heterogeneity being a nuisance factor that needs to be adjusted for, it is empirical evidence of an interaction of treatments with some unspecified subject characteristics when present. When variance heterogeneity is ignored, analysts could interpret the main effects of an experimental study while significant interaction effects (that could be of importance) are concealed. Bryk (1978) suggested that such effects could be substantively interesting and that it could be crucial in evaluating the efficacy of the treatments.

The presence of heterogeneity of variance across the treatment groups is a strong indicator that the treatments have differential effects on individuals. Such effects may cause the mean treatment effect to provide an inadequate summary of the data. It was suggested that sources of heterogeneity must be identified and the treatment effects on the identified interactions be re-estimated. A sequence of analytical activities, as displayed in Figure 2.1, should be followed (Bryk and Raubenbush, 1988). If the homogeneity hypothesis is rejected, the possibility of interaction effects in the experiment should be considered. Assuming that these factors are identified, a new model that incorporates the interaction terms must be fitted and the residual variances must be tested for homogeneity. To reveal the source of the unmeasured interaction effects (e.g. interactions of the treatments with subject characteristics) and their general nature (e.g., equalizing versus disequalizing), post-hoc studies may be conducted. A sequence of steps should be applied if variances are found to be heterogeneous: firstly the variation among the variances could be modelled and then the mean effects could be estimates before the differential effects of the treatments for subjects of differing background could be reported (Bryk and Raubenbush, 1988).

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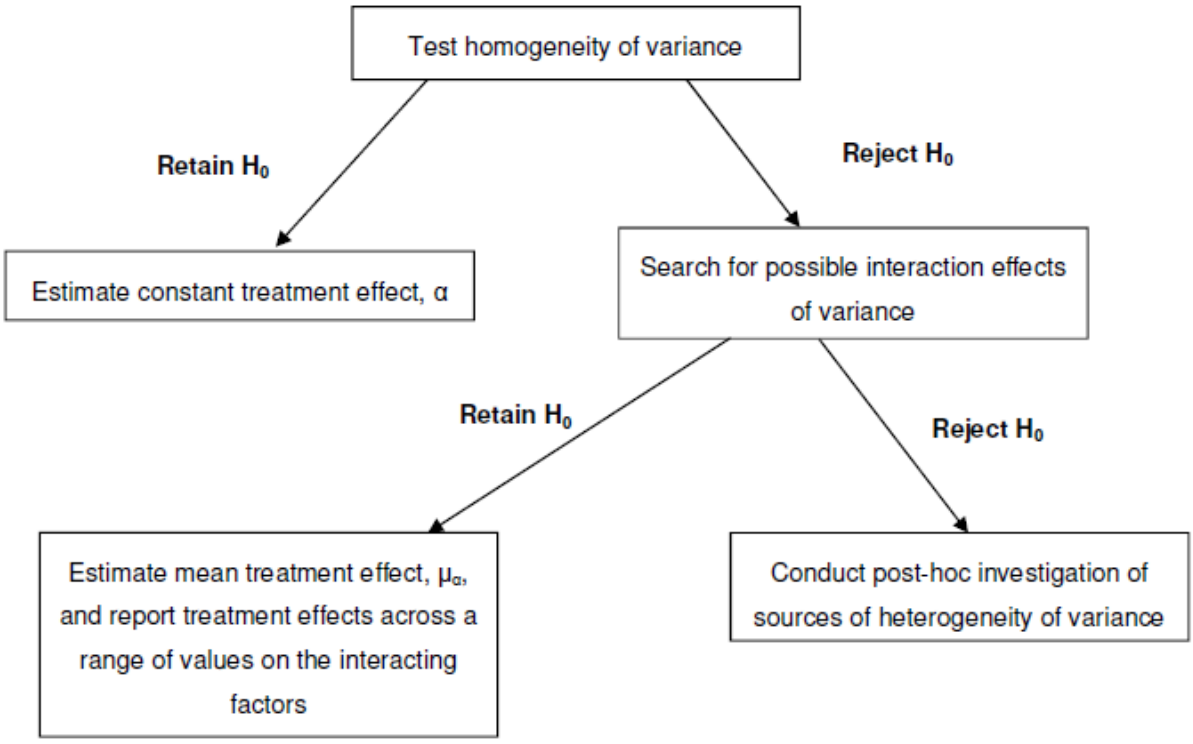

Figure 2.1 Decision tree in analyzing experimental data where it is expected that heterogeneous treatment variances could play a role (Bryk and Raubenbush, 1988).

2.2.2 Heterogeneous variances and genetic evaluations

Against this background, it is necessary to consider the possible effect heterogeneous variance may have on typical animal breeding data stemming from national or international livestock evaluation schemes. In genetic evaluations the assumption is usually made that variances across environments are homogeneous and also that genetic correlations across environments do not differ from unity for a specific trait. In contrast with this assumption, variances for production traits have commonly been found to be heterogeneous across herd or flock classes or in other types of fixed effect levels. Nikolaou *et al.* (2003) mentions of several adjustment methods that have been considered to account for heterogeneous variances. These methods include transformations (mainly transformation to natural logarithms or logarithms to the power of 10), using scaling by the residual or by the phenotypic standard deviation (SD) (Hill, 1984; Weigel and Gianola, 1992) as well as multiple trait approaches (Henderson, 1984). Brown *et al*. (2005) mentions another method whereby traits for individual animals could be expressed as a proportion of their respective contemporary group means. The latter authors also states that this method accommodates heterogeneous residual variances across groups without removing heterogeneous genetic variance across groups. For results to be easily interpreted, it is advisable to transform the individual values back to the observed scale.

Contemporary groups are used to remove environmental biases from genetic evaluations. Such effects could be attributed to differential effects such as management practises associated with grouping (Van Vleck,

1987). Different production environments caused by variable climatic conditions, different pasture species on offer, as well as different feeding regimes under more intensive systems. Differences in raw materials used to formulate diets could also result in differences in production levels as well as in contemporary group means within the data. The within contemporary group variances typical of the data may compromise the estimation of accurate and reliable estimated breeding values (EBV's). Without adjustment the approach of using unadjusted data may lead to EBV's not predicting progeny performance reliably across the different production environments (Brown *et al*., 2005; Huisman and Brown, 2006).

The issue of heterogeneous variances in animal breeding first arose in the dairy animal industries. When examining the effect of heterogeneity of variance in dairy sire evaluations, Winkelman and Schaeffer (1988) as well as Boldman and Freeman (1990) concluded that accounting for heterogeneity did not improve the accuracy of sire evaluations. In a linear model that has been applied by Robert-Granié *et al*. (1999) heterogeneous residual variances was assumed to have known constant ratios and the latter authors contended that accounting for heterogeneous variances had important consequences on the accuracy of EBV's for cows (on the level of cows) but that it had a limited effect on AI bull rankings.

In a study on Lesbos dairy sheep and the impact of variance heterogeneity on genetic evaluations, it was demonstrated that correction for heterogeneity of variance of the fixed effect classes was the most effective method in obtaining the correct genetic evaluations of animals under consideration (Nikolaou *et al.*, 2003). The latter authors also found that the mean of the EBV's of the top sires and dams after adjustment for heterogeneous variances were higher than the mean of the EBV's that was estimated on the raw data. The latter authors furthermore also demonstrated that if only 5-10% of the elite animals were used intensively by artificial insemination (AI), and heterogeneity of variance was not accounted for, the estimation of genetic efficiency would be misleading. In contrast, if natural mating was practiced and if the selection of animals was done on a wider basis (for example selecting sires with positive EBV's and the 20% best dams) the lack of homogeneity of variance was not expected to cause the evaluations to diverge markedly from the theoretically correct ones. In this study, rams were permanently retained in only one flock and their BVs were estimated on their daughters' performance. Under these conditions, it is not unreasonable to expect that the EBVs of the sires could be biased. It seems that the only way to correct the genetic estimations of rams is by using AI, due to the fact that it enables their use in various environmental conditions. Alternatively, the rams could be circulated among flocks following a natural mating scheme. The study done by Nikolaou *et al*. (2003) showed that heterogeneity of variance is caused by reasons associated with flock, lactation number, the number of observations on a specific animal, as well as the production level of the animal.

According to Mostert *et al.* (2006) South Africa has implemented test-day models for the genetic evaluation of production traits in dairy cattle which assumes equal variances of the response variable at different days in milk. The latter authors found that the data used (of Jersey cows from South African Milk Recording Scheme) in these models have higher variances at the beginning and end of the lactation period than in the middle of lactation. They also found that first lactations have a lower mean as well as variance compared to

second and third lactations, which causes deviations in the basic assumption of repeatability models. Mostert *et al.,* 2006) furthermore found that, by pre-adjusting the records of test-day milk, butterfat and protein yield so that the variances are on the same scale, the estimated variance components based on adjusted records were much higher and that the convergence of estimating breeding values was reached significantly faster. They also found significant changes in breeding values and in genetic trends for especially young individual animals. Muasya *et al*. (2007) accordingly found that variance components for milk yield and the magnitude of the estimated breeding values of sires as well as their ranking, for Holstein-Friesian herds in Kenya, are influenced by the production level of the herd.

In a study on Swedish Holstein dairy cattle, Rönnegard *et al.* (2013) found that a change in micro-environmental sensitivity (vEBV) of one genetic standard deviation for either milk yield or somatic cell score would alter the residual variance by 20% in the population. The residual variance could thus be changed by selection of these two previously mentioned traits, but estimates of both estimated breeding values (EBV's) and vEBV requires large data sets. The latter authors also revealed in an economic values investigation that vEBV can be more important than EBV to consider when selecting for a trait within an optimum range in Holstein cattle. Takma and Akbas (2009) stated that accounting for heterogeneity of residual variances is vital for accurate model definition. The latter authors found that by accounting for residual variances in Turkish Holsteins with different schemes caused the estimates at each stage of lactation to vary. Random regression models with more than one residual variance classes are thus recommended to define residual variances through lactation because of their better performance. Different residual variance schemes for the residual variances in random regression models may have a significant effect on the variance components at any of the stages of lactation and should therefore be considered when modelling the effects of residual variances (Takma and Akbas, 2009). Results in a study done on dairy cattle by Liu *et al.* (2007), showed that analyses including a heterogeneous variances approach generally produced a smaller residual variance and thus provided a better fit to the data than when a homogeneous approach was used. This indicates that the heterogeneous approach offers better precision in estimating both the position and effects of QTL mapping. QTL mapping using the heterogeneous approach is useful when based on joint data of diverse reference populations or heteroscedastic data that is obtained from crossing animals with different genetic backgrounds (Liu *et al.*, 2007).

The effect of heterogeneity of variances has not been studied to the same extent in the sheep industry. Brown *et al*. (2005) found in a study conducted on Australian Merino's that transforming body weight and wool data to a proportion of the appropriate contemporary group means resulted in slightly higher heritability estimates, while the resultant EBV's were more robust in terms of predicting progeny performance across different production environments.

It is thus evident that the issue of heterogeneity of variances is commonplace in modern animal breeding (Brown *et al*., 2005). The latter authors showed that correction for heterogeneity of variances resulted in improvements in the accuracy and robustness of breeding values. Correction of data for heterogeneous

variances has so far not been applied to the data of breeds that participate in the NSSIS in South Africa. It is foreseen that similar advantages as those reported by Brown *et al*. (2005) are likely to be achievable in the South African ovine genetic resource population in general and in the local Dohne Merino population in particular. The latter breed has thus been chosen to test whether the same principles apply.

2.3 The use of phantom groups in ovine genetic evaluation

2.3.1 Background on Dohne Merino stud-commercial system

The Dohne Merino Breeder's Society makes use of an open nucleus system (as detailed in Figure 2.2) as an upgrading system to allow two-directional flow of breeding material between stud flocks and commercial flocks. This system has many advantages of which the following are considered as the most important:

- a larger number of animals,
- the possibility of recruiting ewes of greater value in terms of fitness and from the commercial flock,
- a higher selection intensity in the ram breeding nucleus
- and the shortening of the generation interval of ewes, resulting in increased selection gains.

The upgrading system, of which the open nucleus system is part of, represents the most efficient system to ensure that only the sheep with the highest EBV's are taken up in ram breeding flocks. Basically the system was developed with the aim to identify young commercial ewes that is high producing as well as highly adapted that can be selected at a certain stage to move up to the ram breeding flock or stud. Due to the moderate to high repeatability of most production traits as well as presence of additive genetic variation, this system will ensure that a stud that has originated in this way will have a higher production level than any of the original commercial flocks.

The upgrading programme/system consists of four stages (Dohne Merino handleiding, 2009), of which each has his own grade of recording and excellence, namely: the initial stage (base ewes); F1; F2 and F3. The initial stage proposes two original methods of breeding where either Merino ewes or fine wool dual-purpose ewes (including commercial Dohne Merino ewes) are crossed with stud Dohne Merino rams. Group mating of the foundation flock is recommended and the recording of pedigree information of the progeny is not a pre-requisite. However, the flock must first be allocated to the foundation flock register before upgrading of the progeny can take place. At the F1 stage only the female progeny born in the foundation flock register are considered. These ewes must all be clearly and accurately identified by means of ear tags and has to be assessed at 15 to 18 months of age according to the breed standards set by the Dohne Merino Breeder's Society. Group mating of these F1 ewes with approved Dohne Merino stud rams is recommended, and the pedigree records of the progeny is not required. The female progeny of these F1 ewes are considered as the F2 stage. The F2 stage ewes (progeny of F1 ewes mated to Dohne Merino stud rams) need to be inspected according to the breed standards of the Dohne Merino Breeder's Society at 15 to 18 months of age. A

maximum of only the best 60% of these ewes, based upon visual standards as well as on objective measured fleece and body weight traits, will be accredited with the official tag of the F2 generation. The main aim at this stage is to gather as many F2 ewes possible, due to the fact that a small number of their male progeny may be allowed to enter the ram breeding flock. Group mating is recommended at this stage and no pedigree information of the progeny is required. During the F3 stage (when the female progeny of F2 ewes are crossed with Top stud rams – AA in the case of the Dohne Merino) the 20% principle applies. It involves that the F3 ewes will be subjected to inspection on the two-tooth stage and if any of the animals do not meet the breeding standard of the Dohne Merino Breeder's Society they will be culled. Objective measurements of fleece and body weight traits of the F3 ewes is of utmost importance since a maximum of 20% of these ewes will be selected to move up to the stud, as well as the foundation register, based on their performance and adherence to the visual breed standards set by the Dohne Merino Breeder's Society. F3 sheep are accepted as purebred Dohne Merinos once they have been registered in the stud register. These F3 ewes must be mated with individual rams and their progeny must be identified at birth with ear tags. Notifications of the birth of the progeny (male and female) must be submitted to the Dohne Merino Breeder's Society and only after they have been cleared for inspection they will receive the official marking of the Society and be placed on the F4 stud register.

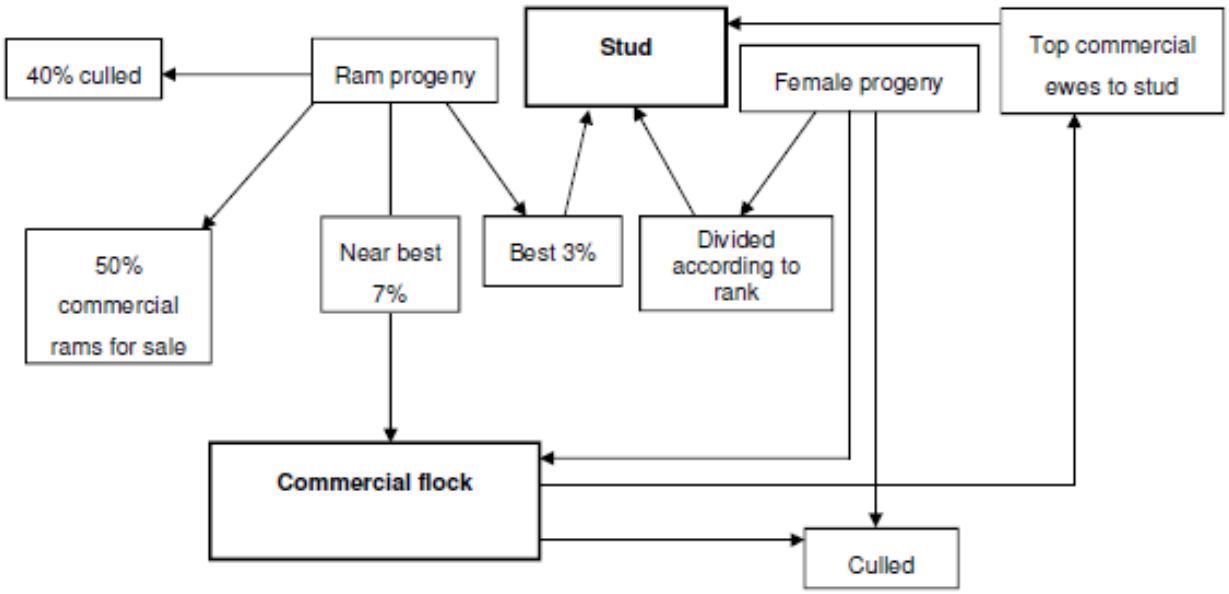

Figure 2.2 The open nucleus system used by the Dohne Merino Breed Society (Dohne Merino Handleiding, 2009)

It is suggested that open nucleus breeding schemes can increase the overall rate of genetic improvement, due to assertive mating with elite animals resulting in a higher proportion of genetically exceptional progeny, compared to closed nucleus systems (Shepherd and Kinghorn, 1992). Mueller and James (1983 and 1984) stated that opening the nucleus to females from the base population increases genetic gains and reduces the relative efficiency of progeny testing, although both effects are small in magnitude. Roden (1995) found that the open nucleus breeding system resulted in higher rates of genetic gain, lower rates of inbreeding and

more predictable selection responses than in closed systems in a simulation study he did by comparing the open and closed breeding systems in a simulated sheep population. The latter author also stated that the initial genetic differences between flocks resulted in higher rates of genetic gain in the open nucleus breeding system due to the use of between flock genetic variance.

Shepherd and Kinghorn (1992) remarked that Mueller and James (1983) recognised that the assumption of constant genetic variance proposed in the early theory of the open nucleus system was unrealistic. According to the latter authors they developed a theory to account for the loss of genetic variation stemming from selection and resulting from the mixing of groups of different breeding values to account for the increase in genetic variance. According to Shepherd and Kinghorn (1992) they showed that the constant variance theory led to an overestimation of genetic gain by up to 20% for traits with a high heritability and by smaller amounts for lowly heritable traits. Mueller and James (1983) accordingly found that the advantage of opening the nucleus and the optimum design were both well approximated by the constant variance theory.

2.3.2 The use of phantom groups

It is important for genetic evaluation to correctly and appropriately deal with animals entering the breeding flock as part of the base population. The concept of phantom groups is commonly used in genetic evaluation of livestock (Theron *et al*., 2002; Fikse, 2009). The concept allows for analysts to correct for the different genetic levels that are present in the herds of flocks by relating base animals to phantom parents (Westall *et al*., 1988).

In South African Holstein cattle the assumption of the animal model that all base animals are sampled from the same population has not been met, due to the importation of semen and herds continually entering performance testing (Theron *et al*., 2002). The latter authors found that the violation of this assumption has led to significant bias in genetic trends for milk, butterfat and protein yield and that the inclusion of phantom parent groups in the model will reduce the bias in the genetic trend to insignificance. It was thus recommended that phantom groups should be incorporated in South African dairy animal genetic improvement, an adaptation to the scheme that has been used since.

So far, no reports on the application of phantom parent groups in the South African ovine genetic resource participating in the NSSIS could be sourced. However, the problem with F3 animals entering the recorded Dohne Merino breeding flock from a commercial base may be dealt with by allocating such animals to a phantom group that is defined in a specific way. The year of birth, country of birth as well as the selection intensity assumed for the phantom parents is usually combined to form phantom parent groups. The year category is included to allow for genetic improvement over time. Schaeffer (2006) stated that phantom parent groups should be assigned according to the four pathways of selection (Sire of Sire, Dam of Sire, Dam of Dam and Sire of Dam), and also by the year of birth of the animal with the unknown parents. Each of the pathways, as mentioned previously, implies different selection intensities on the parent animals. Due to the

lack of the pedigree information from the base population it is sometimes difficult to link imported animals from a country to their common ancestors. These animals may thus be linked to different base animals, which are at different genetic levels due to the improvement that accrued in the population of interest. It is therefore important to create phantom parents to represent the countries and the different time intervals within those countries. Selection intensity differences between breeding lines are another contributing factor to the unequal base levels. According to Westall *et al*. (1988), sires experience much higher selection intensity than dams and thus the selection intensity category is a necessity. These methods need to be assessed under local conditions, to improve the national analysis of the South African Dohne Merino breed. Similarly, it is known that the censoring of data could potentially result in changes in the heritability of traits, with resultant changes in derived breeding values (Donoghue *et al*., 2004; Burns *et al*., 2006).

Mueller and James (1984) stated that the expected genetic gain in an open nucleus system is more rapid, due to increased additive genetic variation (due to differences between tiers constituting the broader industry), but only if substantially more females than males needs to be replaced. The latter authors also stated that the greater selection differential on the dam of sire pathway in the open nucleus system more than compensates for the reduced differential in the sire of dam pathway. Fikse (2009) found that fuzzy-classification (genetic groups of parents are unknown) provides the potential to describe the genetic level of the unknown parents in a more thrifty and structured manner which could increase the precision of the predicted breeding values. In a simulation study the latter authors found that a linear trend in the average genetic level of phantom parents was modelled with a small number of parameters by using fuzzy-classification. It was also found that more complex modelling of the average genetic level of phantom parents was possible by this approach. Solutions for group effects could reflect genetic trends if the animals with unknown parent identifications are a random sample of all contemporary animals within a specific time period (say a specific birth year). Estimated genetic trends will be an average if year groupings are used, while year groupings will also ensure that the groups whereupon genetic trends are based are big enough under most circumstances (Schaeffer, 2006).

2.4 Conclusion

The literature review cited a number of different investigations that have been conducted on dealing with heterogeneous variances and phantom parent groups. There is a lack of studies on these topics that involves sheep, highlighting the importance of the following studies that have been supported by the local wool industry. Studies on sheep that were cited in the review were mostly conducted under Australian conditions and involved breeds other than the Dohne Merino. It is foreseen that this research will benefit the Dohne Merino sheep breed and improve the accuracy of EBV's when heterogeneous variances are accounted for, as well as when phantom parents are incorporated into the NSSIS analysis to scientifically deal with F3 parents entering the recorded industry from a commercial base.

It was suggested that taking heterogeneous variances into account, and adjusting for it by means of an appropriate transformation, would improve the accuracy and robustness of breeding values in important

production traits. Dohne Merino breeders furthermore place a high value on animals entering the breeding flock from a commercial base, as it is suggested that these animals assist with maintaining the fitness of the flock. Yet the EBV's of such animals are often underestimated, as they do not carry any pedigree information. By relating base animals with no pedigree to phantom parents the different genetic levels within the tiers of the national flock can be corrected for. This study is expected to show the effect of using an appropriate transformation and appropriately assigning F3 progeny to phantom parent groups on EBV's for the important production traits (body weight, clean fleece weight and fibre diameter) of the Dohne Merino breed in South Africa. Genetic trends resulting from these EBV's are also experceted for benefit from these adaptations to the NSSIS analysis.

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Chapter 3

The effect of heterogeneity of contemporary group variances on the accuracy of breeding values and genetic trends for the Dohne Merino

W. Jordaan[1], S.W.P. Cloete[1,2], J.J. Olivier[2] and K. Dzama[1]

[1] *Department of Animal Sciences, University of Stellenbosch, Matieland, 7600*

[2] *Department of Animal Production, Elsenburg, 7607*

Abstract

The South African Dohne Merino Breeder's Society has in latter years moved genetic evaluations from within flock to across flocks. Due to this as well as the diverse environments in which selection takes place, the accuracy of derived breeding values may be affected. Contemporary groups (consisting of Flock-Year-Season-Sex-Management group) have been constructed to account for the vastly different environments, and transformations were done on body weight, clean fleece weight and fibre diameter data to account for the possible heterogeneity of contemporary group variances. Direct heritability estimates for these traits were 0.265 (0.005) for body weight, 0.210 (0.004) for clean fleece weight and 0.437 (0.005) for fibre diameter. Interactions of sires with contemporary groups constituted approximately 2% of phenotypic variance for all three traits; thus large-scale re-ranking of sires across environments was not likely. Furthermore, sires were allocated to High and Low groups, based on the phenotypic means of their flocks of origin, to determine if transformation would lead to adjustments in their breeding values. Scatter-plots and derived regression information showed that transformation lead to the breeding values in the sires origination from High group flocks being adjusted downwards and the sires from Low group flocks upwards. Genetic trends for the three traits revealed that the transformation had a profound effect on body weight and clean fleece weight Fibre diameter was affected to a lesser extent by the transformation. It is recommended that the transformations described are applied routinely.

Keywords: Heterogeneous variances, contemporary groups, estimated breeding values

3.1 Introduction

The Dohne Merino Breed Society calculated the BLUP of breeding values for registered breeders on a within-flock basis since the 1990's. The grading of animals was performance-based on a computerized flock-recording scheme introduced in 1985, based on the index system. Genetic evaluations in the breed have been changed from a within-flock to an across-flock basis in the breed to enhance overall genetic progress (Delport *et al*., 2003).

Data used for the genetic evaluation of Dohne Merino sheep originated from a wide range of environments in South Africa. South Africa is known for its diverse environments, ranging over nine different biomes as well as five different aridity zones (Palmer and Ainslie, 2006). Marked differences in production levels and contemporary group means therefore occur in the data. These differences have implications for the within contemporary group means of the data, and are likely to affect the estimated breeding values (EBV's) if not

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properly accounted for by linkages among flocks at all levels of the industry. Animals from groups with higher means are likely to have greater variation in their EBV's. If these variations in EBVs are not properly adjusted for, progeny performance will not be reliably predicted across the different production environments (Brown *et al*., 2005).

Heterogeneous genetic variance across groups can occur when the genetic differences are expressed more in superior environments when compared to inferior environmental conditions (Brown *et al*., 2005). To avoid these problems, a transformation is needed where individual performance for traits is expressed as a proportion of contemporary group means. This method was also used by Brown *et al*. (2005). Nikolaou *et al*. (2003) suggested several other adjustment methods that may be appropriate to account for heterogeneous variances. These include transformations (mainly log or square root transformations), scaling by the residual or by the phenotypic standard deviation (Hill, 1984; Weigel and Gianola, 1992), as well as multiple-trait approaches (Henderson, 1984), where performance in different environments are modelled as different traits. Henderson (1975) stated that if heterogeneity is ignored, it may reduce the reliability of ranking and selection procedures based on the Henderson's mixed model equations (as seen in Reverter *et al*., 1997), which requires appropriate variance components to provide solutions with BLUP properties. Based on a study on carcass traits of beef cattle, Reverter *et al*. (1997) stated that correction for heterogeneity resulted in heritability estimates increasing by an average of 4.2% for all the traits. Due to South Africa's diverse environment, animals expressing vastly different production levels are likely to be maintained in the different contemporary groups contributing data to national analyses. The question therefore arises whether the analysis of non-transformed data would lead to an overestimation of breeding values in those animals maintained in contemporary groups with higher means (and arguably higher levels of variation).

The aim of this study was therefore to determine the effect of transforming data to account for the heterogeneity of contemporary group variances for body weight, clean fleece weight and fibre diameter in the South African Dohne Merino breed analysis.

3.2 Materials and Methods

3.2.1 Data

Performance records and pedigree information for this study were obtained from the National Small Stock Improvement Scheme (NSSIS) database, and consisted of records of lambs born during a 20-year period between 1992 and 2011. The original data set consisted of 301 290 records and included animals with records for body weight, clean fleece weight and fibre diameter.

To compensate for the variable environmental conditions during genetic analyses, animals raised similarly were assigned to uniform groups known as contemporary groups. According to Van Vleck (1987), contemporary groups are also used to remove biases from genetic evaluations due to differential effects,

such as, the management associated with the grouping. In the current study, the contemporary groups were created by concatenating flock-year-season-sex-management group (FYSSM). The year and season in the contemporary group refers to the year and season of birth of the animal. These contemporary groups have been defined by the breeder responsible for submitting the data. Since management styles of the different breeders may be different, the record-keeping for all registered Dohne Merino breeders has been standardised according to guidelines published by the Dohne Merino Breeder's Society (Dohne Merino Manual, 2009).

The data were analysed either without being transformed to account for heterogeneous contemporary group means, or after transformation according to the method described by Brown *et al*. (2005), where the performance of individual animals for each trait was expressed as a proportion of the contemporary group (CG) mean. After this transformation was effected the individual records were transformed back to the observed scale by expressing them in relation to the overall phenotypic mean. The Sire-flock-season interaction was included in the analyses to increase the fit of the model and also to enhance the accuracy of sire rankings.

Only records of animals recorded for all the three traits (body weight, clean fleece weight and fibre diameter) were used. This resulted in a final data set containing 282 513 records, which were the progeny of 5 698 sires and 105 886 dams across 20 years (1992 to 2011) and situated in 6 291 contemporary groups.

3.2.2 Statistical analyses

The statistical analysis was divided into four sequential steps. The final data set were first analysed using GenStat (Payne *et al*., 2011) to obtain summary statistics for the three traits before and after transformation. This analysis was needed to assess the effect of the transformation on the statistical properties in terms of the distribution of the data.

Secondly, a three-trait animal model analysis was developed to estimate (co)variance components. The ASReml programme (Gilmour *et al*., 2009) was used for this purpose. These estimates were then used to estimate genetic parameters, such as heritability of the traits, as well as the genetic and phenotypic correlations among the traits. Animal solutions emanating from this analysis were used as predicted breeding values for the animals for all traits in the three-trait model. The genotype by environment interaction was modelled by the inclusion of an additional random factor, namely the sire-flock-season (SFS) interaction. Meyer (1987) stated that such interactions reflect both common environmental effects and interactions. Brown *et al*. (2009) found that sire by flock-year interaction effects significantly improved the fit of the model and resulted in a direct-maternal genetic correlation closer to zero in Poll Dorset sheep.

Fixed effects for this model were estimated with the SAS Enterprise Guide program (SAS, 2007) in a general linear model (GLM) to assess the effect of each main effect on each of the three traits analysed. Dam age

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and age of the animal at recording were used as covariates. The fixed effects and these covariates that were included in the model and were accounted for as sources of variation were the following:

Age Age of the animal at performance measurement. This effect was plotted as a polynomial; thus only the slope and no intercept. It can also be defined as a term with two columns having centred and scaled linear coefficients in the first column, and centred and scaled quadratic coefficients in the second column (ASReml User Guide, Gilmour *et al*., 2009).

AgeDam The age of the dam, ranging from one to ten years of age was plotted as a linear regression

BStat The rearing type of the animal, ranging from single, twins or triplets.

CG The contemporary group which was defined previously as FYSSM.

The following mixed model equation was used:

$$\mathbf{y = Xb + Z_1a + Z_2sfs + e}$$

where **y** is a vector of observations for body weight, clean fleece weight and fibre diameter
b is a vector describing all the fixed effects in the model
a is a vector of direct additive genetic effects
sfs is a vector of sire x flock x season interaction effects
X, Z_1, Z_2 are incidence matrices relating data to the above vectors, respectively, and
e is a vector of residuals

With **A** being the numerator relationship matrix and **I** an appropriate identity matrix, the following was assumed:

$$V(a) = A\sigma^2_a; V(c_{sfs}) = I\sigma^2_{sfs}; V(e) = I\sigma^2_e$$

where, and σ^2_a, σ^2_{sfs} and σ^2_e is the direct genetic variance, sire-flock-season variance and environmental residual) variance respectively.

The following (co)variance estimates and ratios were calculated as:

1. Phenotypic variance is defined as
   $\sigma^2_p = \sigma^2_a + \sigma^2_{sfs} + \sigma^2_e$

2. Heritability for the direct additive genetic effect
   $h^2_a = \sigma^2_a / \sigma^2_p$

3. Sire-flock-season (SFS) variance as proportion of total phenotypic variance
   $c^2_{sfs} = \sigma^2_{sfs} / \sigma^2_p$

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4. Genetic and phenotypic correlations among the three traits considered (body weight, clean fleece weight and fibre diameter)
   $r_{ab} = \sigma_{ab} / \sqrt{\sigma_a^2 \sigma_b^2}$

ASReml employs an average information algorithm that concomitantly derives standard errors for those variance ratios of interest, such as correlations and heritability estimates.

Raw data were also divided on approximate thirds into high, medium and low groups based on the phenotypic means of the flocks included in the analysis. The objective of this exercise was to assess the effect of heterogeneity of contemporary group variances on the ranking of sires. It was assumed that the effect of transforming data to account for heterogeneous variances would have the largest impact on the extreme flocks in terms of phenotypic production levels. Sires originating from the medium flocks were thus not considered further, and further analyses focussed on those sires that originated from high and low flocks. Phenotypic means for these arbitrary groups were derived, using the software program, SAS Enterprise Guide (SAS, 2007). Only animals from well-linked flocks were used for this part of this study. This implies that ± 5 000 records of the poorly linked flocks were not considered even though the direction and overall magnitude of differences between the high and low groups in the poorly linked flocks concurred with the well-linked flocks (containing more than 65 000 records).

Sire estimated breeding values stemming from the analysis of transformed data were regressed upon their breeding values derived from non-transformed data for sires originating from both the top third flocks (n=146) and bottom third flocks (n=180). A combined equation, encompassing sires originating from both top and bottom third of flocks, was also generated with SAS Enterprise Guide Software (SAS, 2007) for each of the traits. Under conditions where the transformation had no effect whatsoever, the slope (regression coefficient) would be equal to one and the intercept would be equal to zero, namely $\mathbf{y = x}$. There would also be no difference between regressions derived for the top third and bottom third flocks. The transformed data would therefore be equal to the non-transformed data and no adjustment would be necessary, irrespective of the placement of the flock of origin in the top third or in the bottom third based on the overall phenotypic means. To determine if the graphs differ between groups (High and Low) for specific traits, their standard errors were used to compare intercepts and slopes where appropriate.

Finally, genetic trend analyses were completed for the respective traits in the High and Low groups (transformed and non-transformed data) to obtain regression equations as well as correlation coefficients.

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3.3 Results and discussion

3.3.1 Descriptive statistics

From Table 3.1, it is evident that the transformation resulted in substantially reduced coefficients of variation. This is particularly true for body weight and clean fleece weight, where the derived coefficients of variation more than halved. The coefficients of variation for non-transformed traits were consistent with those of Van Wyk *et al*. (2008), namely 25% for body weight, 34% for clean fleece weight and 8% for fibre diameter. These authors also analysed non-transformed data emanating from the national Dohne Merino breed analysis across flocks. In contrast, Cloete *et al*. (1998) reported generally lower coefficients of variation in their within-flock analysis of the Kromme Rhee Dohne Merino flock, namely 18% for body weight, 20% for clean fleece weight and 6% for fibre diameter. These values are in closer resemblance of the values derived from the transformed data in the present study. Corresponding coefficients of variation in seven Australian Merino research resource flocks used for across-flock analyses ranged from 16.7 to 22.2% for yearling body weight, from 18 to 31% for clean fleece weight, and from 8.7 to 11.1% for fibre diameter (Safari *et al*., 2007). These results are fairly consistent with results from the current study for non-transformed data.

Table 3.1 Summary statistics for the transformed data and for non-transformed data for body weight, clean fleece weight and fibre diameter

Para-meter	Body weight		Clean fleece weight		Fibre diameter	
	Non-transformed	Transformed	Non-transformed	Transformed	Non-transformed	Transformed
Mean	50.81	50.72	3.02	3.09	18.90	18.91
SD	12.94	4.86	1.11	0.46	1.67	1.15
SE of mean	0.02	0.01	0.02×10^{-1}	0.08×10^{-2}	0.03×10^{-1}	0.02×10^{-1}
Variance	167.60	23.57	1.23	0.22	2.78	1.33
CV	25.47	9.57	36.65	15.03	8.82	6.09
Min	20.00	25.46	0.50	1.24	12.60	13.37
Max	103.00	80.88	10.07	5.24	26.00	26.28

Distributions for transformed (T) and non-transformed (NT) data were then considered to assess the effect of transforming data to percentages on the data properties. The distribution of body weight is presented in Figure 3.1. It is evident that the transformed data for body weight are better distributed, as can also be deducted from the parameters reported in Table 3.1. It can thus be hypothesised that transformed values should probably be used during the analysis of body weight data.

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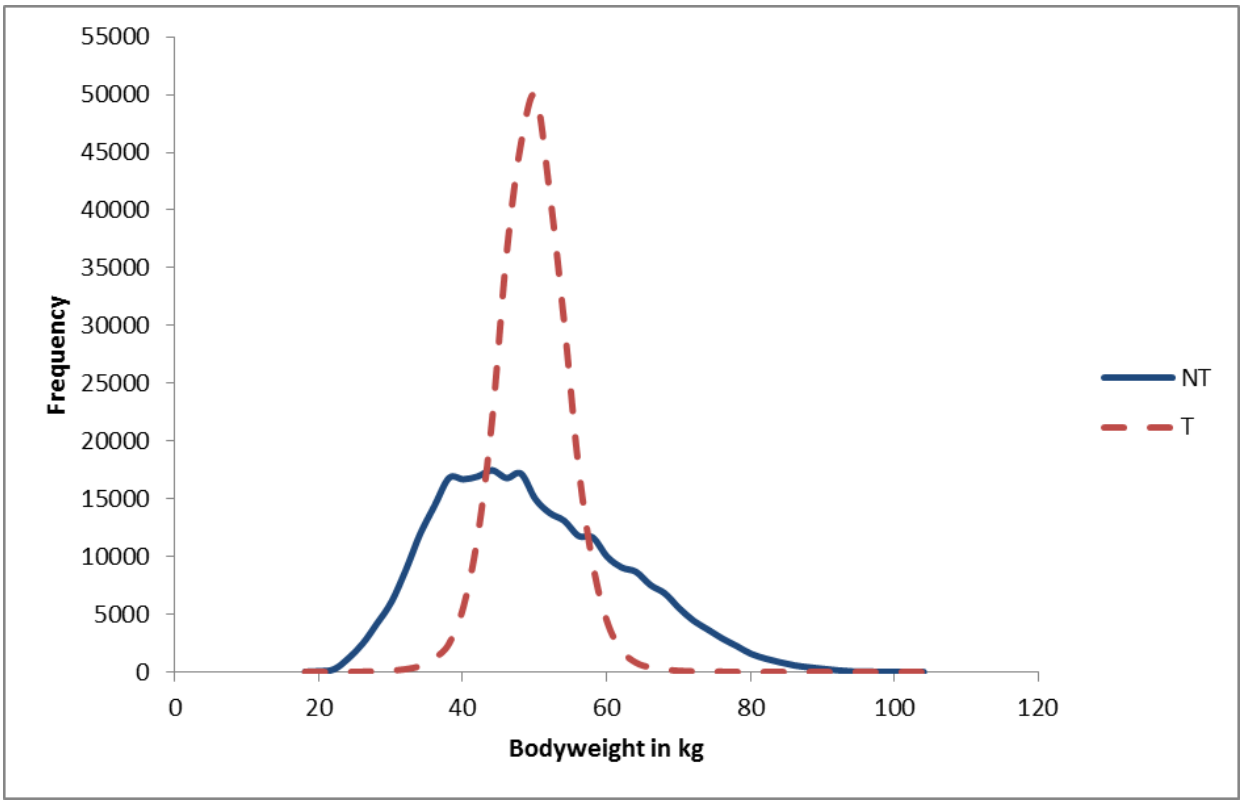

Figure 3.1 Distribution of body weight of 282 513 individuals with and without the transformation described in the Material and Methods (NT – Non-transformed; T – Transformed)

In Figure 3.2 the distribution of clean fleece weight, transformed and non-transformed, are presented. It is evident that the transformed data for clean fleece weight were appreciably better distributed than non-transformed data, and should be preferred for further analysis. This assessment is also supported by the summary statistics reported in Table 3.1.

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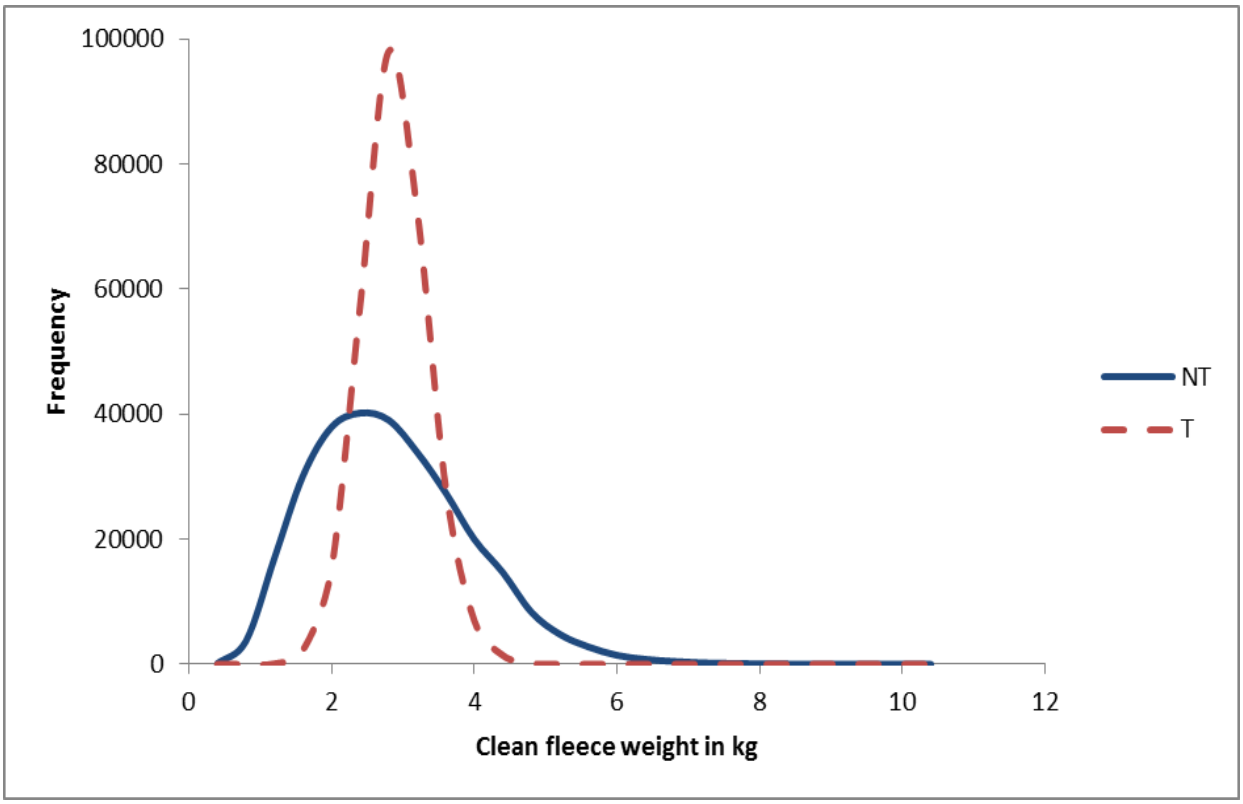

Figure 3.2 The distribution of clean fleece weight of 282 513 individuals with and without the transformation described in the Material and Methods (NT – Not transformed; T – Transformed)

The distributions of fibre diameter for transformed and non-transformed data are presented in Figure 3.3. It is obvious that the transformation of data to percentages had a substantially reduced effect upon the distribution of fibre diameter data, when compared to the effect transformation had on body weight and clean fleece weight data. This deduction is also supported by the information supplied in Table 3.1.

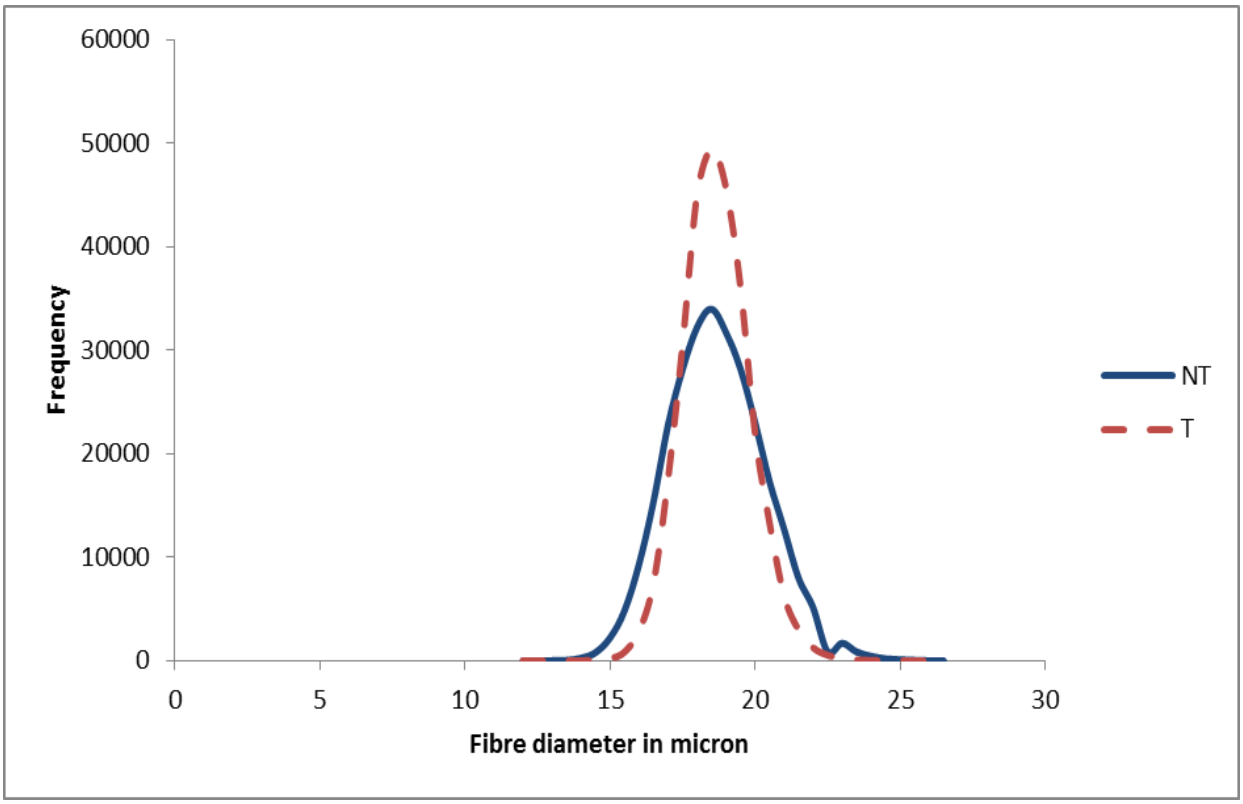

Figure 3.3 The distribution of fibre diameter of 282 513 individuals with and without the transformation described in the Material and Methods (NT – Non-transformed; T – Transformed)

3.3.2 Multivariate analysis

3.3.2.1 Heritability estimates

The heritability of body weight was estimated at 0.265 from the three-trait analysis using transformed data (Table 3.2). This value is appreciably higher than the previous estimate of 0.17 reported for the Dohne Merino breed by Van Wyk *et al*. (2008), using non-transformed data. However, it needs to be conceded that the latter analysis also included maternal genetic effects (0.01) and maternal permanent environment effects (0.03) for body weight. Safari *et al*. (2005) accordingly reported a heritability of 0.31 (0.03) for dual-purpose sheep in their extensive review on genetic parameters for sheep. Previous heritability estimates for body weight in Dohne Merino sheep included values that were comparable to the present estimate, namely 0.28 (Swanepoel, 2006) and 0.24 (Cloete *et al*., 1998). Other heritability estimates reported for wool sheep in literature included values of 0.25 (Erasmus *et al*., 1990), 0.49-0.52 (Duguma *et al*., 2002), 0.41 (Safari *et al*., 2005), 0.35 (Olivier and Cloete, 2007) and 0.41-0.44 (Huisman *et al*., 2008). Brash *et al*. (1994) obtained a heritability of 0.13 for yearling body weight in Corriedale dual-purpose sheep. It is evident that the present value is well within the ranges of these estimates.

The heritability estimate for clean fleece weight was 0.21, when using transformed data. Comparable estimates in literature included an estimate of 0.51 for dual-purpose sheep (Safari *et al*., 2005). Heritability

estimates previously reported for clean fleece weight in Dohne Merino sheep were 0.35 (Cloete *et al*., 1998), 0.22 (Swanepoel, 2006) and 0.19 (Van Wyk *et al*., 2008). For wool sheep, the following values were reported: 0.23 (Erasmus *et al*., 1990), 0.36 (Safari *et al*., 2005), 0.29 (Olivier and Cloete, 2007), 0.18-0.26 (Huisman *et al*., 2008), 0.32 (Banks and Brown. 2009) and 0.38 (Mortimer *et al*., 2009). Brash *et al*. (1994) observed a heritability estimate 0.29 in Corriedales. The present heritability estimate is well within this range of values.

Fibre diameter was moderately heritable at 0.437, which is consistent with previous estimates for Dohne Merinos (Cloete *et al*., 1998; Swanepoel, 2006; Van Wyk *et al*., 2008). Safari *et al*. (2005) derived values of 0.57 for dual-purpose breeds and 0.59 for wool breeds from the literature. Other estimates for wool breeds in literature included values of 0.55, 0.62-0.77, 0.62 and 0.65, respectively, obtained by Olivier and Cloete, (2007), Huisman *et al*. (2008), Banks and Brown (2009) and Mortimer *et al*. (2009). Brash *et al*. (1994) reported estimates of 0.56 for yearling fibre diameter and 0.62 for hogget fibre diameter in Corriedale sheep. It thus seems that, while the correspondence between estimates involving Dohne Merinos is very good, derived heritability estimates for fibre diameter in the present study were somewhat lower than most literature estimates on other wool breeds, mostly Merinos.

Brown *et al*. (2005) found that by transforming the data for body weight, clean fleece weight and fibre diameter to a proportion of their contemporary group mean has beneficial outcomes for genetic evaluation. In the current study, these beneficial outcomes included a slightly higher heritability in the transformed data. Thus, the estimated breeding values may become more robust in terms of predicting progeny performance across different production environments.

The sire-flock-season variance ratios, namely 0.017 (0.001) for body weight, 0.020 (0.001) for clean fleece weight and 0.026 (0.001) for fibre diameter, were very low. Swanepoel (2006) found a comparable variance ratio for fibre diameter of 0.027. The sire-flock-year-season variance ratios in the study by Van Wyk *et al*. (2008) were also quite similar, accordingly amounting to about 2% of the phenotypic variation for all traits. Therefore, the genotype by environmental interactions is not very important in Dohne Merinos; hence the ranking of sires is likely to be fairly stable, except for mediocre sires.

Table 3.2 Estimates of variance components and ratios (SE in brackets), as well as direct heritability (in bold on the diagonal), genetic correlations (below the diagonal) and phenotypic correlations (above the diagonal) obtained from the three-trait analysis using transformed data

	Body weight (BW)	**Clean fleece weight (CFW)**	**Fibre diameter (FD)**
Variance components			
Phenotypic	24.655	0.223	1.468
Residual	17.691	0.172	0.789
Direct additive	6.534	0.047	0.641
Sire-herd-season	0.430	0.004	0.038
(Co)variance ratios			
Sire-flock-season	0.017 (0.001)	0.020 (0.001)	0.026 (0.001)
BW	**0.265 (0.005)**	0.327 (0.002)	0.150 (0.002)
CFW	0.035 (0.015)	**0.210 (0.004)**	0.190 (0.002)
FD	0.139 (0.011)	0.169 (0.012)	**0.437 (0.005)**

3.3.2.2 Correlations

The genetic correlations among the traits analysed are presented in Table 3.2. Body weight had a genetic correlation of 0.035 (0.015) with clean fleece weight. Swanepoel (2006) reported a comparable correlation of 0.05 for this correlation, while Van Wyk *et al*. (2008) reported a somewhat higher genetic correlation of 0.11 in their analyses of the national Dohne Merino breed. In wool breeds, Safari *et al*. (2005) derived a higher value of 0.11 from the available literature, while Olivier and Cloete (2007) found a much higher value of 0.27 in a breed analysis on South African Merino sheep. The estimated genetic correlation between body weight and fibre diameter was estimated at 0.139 (0.011), which is similar to previous estimates for the Dohne Merino breed (Swanepoel, 2006; Van Wyk at al., 2008). Higher estimates of 0.18 and 0.16 were reported by Safari *et al*. (2005) and Olivier and Cloete (2007), respectively, in wool breeds. A low genetic correlation of 0.169 (0.012) was estimated between clean fleece weight and fibre diameter in the present study. Similar values were reported by Swanepoel (2006) and Van Wyk *et al*. (2008) in their analyses of the Dohne Merino in a previous breed analysis. Safari *et al*. (2007) reported higher values of 0.29 for wool breeds and 0.28 for dual-purpose breeds based on their comprehensive review of literature genetic parameter estimates for sheep. A lower estimate of 0.06 for Merinos was obtained by Erasmus *et al*. (1990), while estimates of 0.18 for Afrinos and 0.20 for Merinos were observed by Snyman *et al*. (1998) and Olivier and Cloete (2007), respectively.

From these results, it is evident that the derived parameters are mostly consistent with those previously derived during breed analyses on Dohne Merinos (Swanepoel, 2006; Van Wyk *et al*., 2008). This is perhaps not surprising, as the bulk of the data were undoubtedly common to all analyses. It is nevertheless

interesting to note the good correspondence between studies if the data were transformed to proportions, as suggested by Brown *et al*. (2005), while the previous studies by Swanepoel (2006) and Van Wyk *et al*. (2008) were based upon non-transformed data.

Laas (1982) stated that live weight, clean fleece weight and fibre diameter could be regarded as being the most important traits to be considered during selection of the Dohne Merino. Van Wyk *et al*. (2008) considered the comparatively low genetic correlations in the Dohne Merino among body weight, clean fleece weight and fibre diameter, and suggested that these correlations may suggest that wool quality and quantity may not be compromised if selection is targeted at improving meat production in this breed.

Table 3.2 shows the phenotypic correlations which were generally low to medium. The phenotypic correlation between body weight and clean fleece weight of 0.327 (0.002) was similar to previous estimates on Dohne Merino (Swanepoel, 2006; Van Wyk *et al*., 2008). It is interesting that this estimate is considerable higher than the corresponding genetic correlation. In wool breeds, lower values of 0.07 and 0.24 were, respectively, obtained by Olivier and Cloete (2007) and Safari *et al*. (2005). In contrast to the phenotypic correlation between body weight and clean fleece weight, the other phenotypic correlations involving fibre diameter were much more comparable in magnitude to the corresponding genetic correlations. The phenotypic correlation estimated between body weight and fibre diameter was 0.150 (0.002). Swanepoel (2006) reported a comparable estimate of 0.129 (0.004) as did Van Wyk *et al*. (2008) with a recorded value of 0.131 (0.004). Olivier and Cloete (2007) obtained a slightly higher value of 0.19 in Merinos, while Safari *et al*. (2005) reported a negative value of -0.05 for wool breeds. Clean fleece weight had a phenotypic correlation of 0.190 (0.002) with fibre diameter, which was similar to previous estimates (Swanepoel, 2006; Van Wyk *et al*., 2008). Slightly higher estimates (0.25, 0.25 and 0.24) were obtained by Safari *et al*. (2005), Olivier and Cloete (2007) and Safari *et al*. (2007), respectively. A higher value of 0.25 was reported for dual-purpose breeds by Safari *et al*. (2005). Studies on Merinos produced estimates of 0.24 and 0.25 (Olivier and Cloete, 2007; Safari *et al*., 2007).

Overall the genetic and phenotypic correlations were all generally low to moderate and positive. These results will thus suggest that selection for a bigger or heavier animal will result in gradual increase in the amount of wool collected as well as an increase in fibre diameter. Selecting for higher clean fleece weight will also lead to gradual increase in fibre diameter.

3.3.3 High and Low groups

Data used for genetic evaluation of the Dohne Merino originates from a vast array of genotypes and environments across South Africa, which may result in large differences in the level of production and contemporary group means within the data. According to Brown *et al*. (2005), estimated breeding values may not reliably predict progeny performance across different production environments if the groups with higher means; and hence higher levels of variance, are not adjusted. To evaluate the effect of transformation

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on estimated breeding values, sires from the top third (High group) and bottom third (Low group) of the flocks comprising the national flock were divided into High and Low groups (based upon their level of production) for each of the three traits. This was also done to determine what adjustment should be made, taking into account the transformation of the data, concerning the High and Low groups.

3.3.3.1 Phenotypic characterization

Since the allocation of flocks to the High and Low groups can be somewhat arbitrary, these groups were characterized in Table 3.3. The allocation had a marked influence on the means of the High and Low flocks, particularly as far as body weight and clean fleece weight were concerned. Expressed relative to the means of the Low flocks, the High flocks exceeded the latter group by 53% for body weight and by 70% for clean fleece weight. The corresponding difference for fibre diameter amounted to 6%, which is comparatively small. Previous research accordingly suggested that fibre diameter is not affected to the same extent by environmental influences as live weight and clean fleece weight in particular (Grobbelaar *et al*., 1990; Cloete *et al*., 1992).

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Table 3.3 Raw phenotypic means (± SD), coefficients of variation and ranges for animals occurring in the High and Low flocks for the respective traits

Trait and allocation	Number of observations	Mean ± SD	Coefficient of variation (%)	Range
Body weight (kg)				
High	41665	60.8 ± 11.4	18.8	29 – 103
Low	29631	39.7 ± 8.3	20.9	20 – 90
Clean fleece weight (kg)				
High	38598	3.87 ± 1.10	28.4	0.50 – 7.03
Low	28852	2.27 ± 0.67	29.5	0.70 – 9.94
Fibre diameter (micron)				
High	39078	19.7 ± 1.6	8.1	12.6 – 26.0
Low	28751	18.5 ± 1.5	8.1	14.4 – 26.0

3.3.3.2 Genetic trends

Regression coefficients for sires that originated from the High and Low groups for each of the three traits (body weight, clean fleece weight and fibre diameter) will be discussed individually. The combined equation, for the High and Low group values, for each of the three traits (Table 3.4) will also be mentioned briefly to introduce this discussion.

Table 3.4 Intercepts, slopes (SE in brackets) and coefficients of determination (R^2) depicting the regressions of breeding values based on transformed data on breeding values based on non-transformed data.

	Body weight	**Clean fleece weight**	**Fibre diameter**
R^2	0.874	0.621	0.942
Coefficients			
Intercept (a) (SE)	0.214 (0.055)	0.016 (0.006)	-0.002 (0.008)
Slope (b) (SE)	0.960 (0.020)	0.699 (0.030)	1.010 (0.014)

Brown *et al*. (2005) reported that the regression of progeny performance on sire estimated breeding values on levels of production from Low to High were significant for all of the traits. They also stated that transforming the traits to the proportion scale largely removed the trends in regression coefficients and also produced estimated breeding values that were more reliable across different production environments.

3.3.3.2.1 Body weight

Statistics for the combined data describing the regression of breeding values based on transformed data on breeding values based on non-transformed data for body weight in Table 3.4 indicate that the intercept were higher than zero. The regression coefficient (slope), on the other hand, was on the boundary of being different from one.

When individual data depicting the regressions of sire breeding values based on transformed body weight data on breeding values based on non-transformed data for the sires originating from the High and Low flocks were compared, the slopes and intercepts differed according to classification (Table 3.5). The High group was characterised by an equation with an intercept below zero and a slope below one. In contrast, the Low group had an intercept above zero a slope above one. A scatter-plot depicting these relationships is provided in Figure 3.4. The information supplied in Table 3.5 and Figure 3.4 suggest that sire breeding values in those sires originating from flocks in low environments would be adjusted upwards by transforming body weight data according to the method described by Brown *et al*. (2005). In contrast, breeding values for sires from High flocks would be adjusted downwards.

In an ideal situation the slope will be equal to one and the intercept will be equal to zero so that the transformation would lead to no adjustments being made regarding the breeding values of the sires. The results found for body weight, suggested that the sire breeding values will be adjusted upwards or downwards due to the transformation for Low and High flocks respectively. This result supports the statement made by Brown *et al*. (2005) that by transforming the trait to the proportion scale largely removes the trends in the regression coefficients and also produces estimated breeding values that are more reliable across different production environments.

Table 3.5 Regression equations (SE in brackets) of transformed breeding values on non-transformed breeding values for sires classified as originating from the High and Low flocks for body weight

Classification	Intercept (a) with SE	Slope (b) with SE	Residual Mean Square	R^2	Number of observations
High	-0.143 (0.067)	0.911 (0.020)	0.213	0.936	146
Low	0.417 (0.042)	1.256 (0.022)	0.283	0.950	180

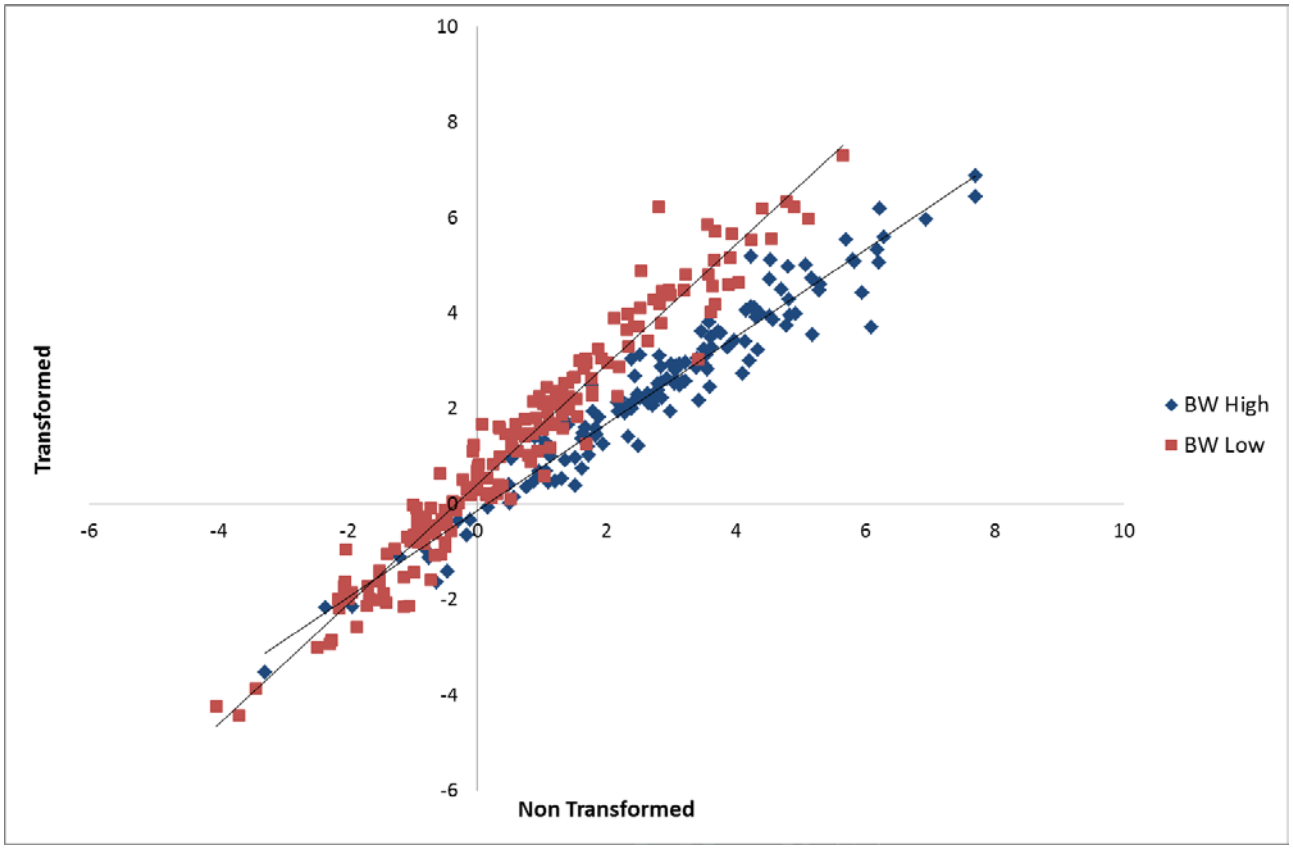

Figure 3.4 Scatter-plots depicting the regressions of sire breeding values based on transformed data on breeding values based on non-transformed data for body weight in sires originating from High or Low environments respectively

3.3.3.2.2 Clean fleece weight

Statistics for the combined data describing the regression of breeding values based on transformed data on breeding values based on non-transformed data for clean fleece weight (Table 3.4) indicate that the intercept differed from zero. On the other hand the regression coefficient (slope) was much lower than one.

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When comparing individual data depicting the regressions of sire breeding values based on transformed clean fleece weight data on breeding values based on non-transformed data for the sires originating from the High and Low flocks, slopes and intercepts differed considerably according to classification (Table 3.6). The data for the High group had an intercept below zero and a slope below one, as was also the case for body weight. The Low group had an intercept above zero and a slope above one, which was also found for body weight. Sire breeding values, as shown in Table 3.6 and Figure 3.5, in the sires that originated from flocks in Low environments would be adjusted upwards by the transformation of clean fleece weight data according to the method described by Brown *et al*. (2005). In contrast, breeding values for sires originating from High flocks would be adjusted downwards.

It is evident that the transformation of clean fleece weight to the proportion scale largely removed the trends in regression coefficients of the High and Low flocks and also produced estimated breeding values that were more reliable across different production environments. This finding is consistent with results previously reported by Brown *et al*. (2005).

Table 3.6 Regression equations (SE in brackets) of transformed breeding values on non-transformed breeding values for sires classified as originating from the High and Low flocks for clean fleece weight

Classification	**Intercept (a) with SE**	**Slope (b) with SE**	**Residual Mean Square**	**R^2**	**Number of observations**
High	-0.043	0.690	0.004	0.815	146
	(0.007)	(0.027)			
Low	0.081	1.259	0.004	0.844	180
	(0.005)	(0.040)			

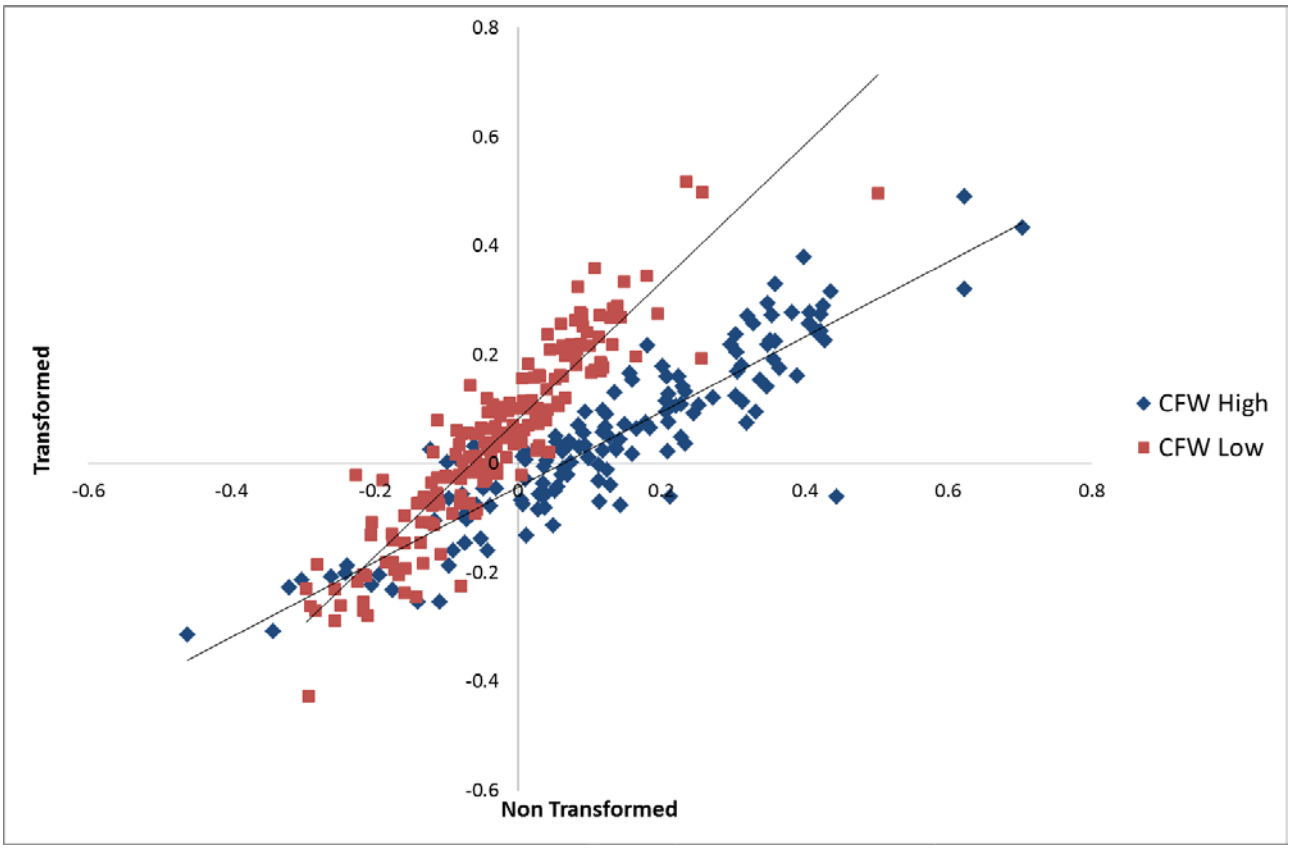

Figure 3.5 Scatter-plots depicting the regressions of sire breeding values based on transformed data on breeding values based on non-transformed data for clean fleece weight in sires originating from High or Low environments

3.3.3.2.3 Fibre diameter

Combined data statistics describing the regression of breeding values based on transformed data on breeding values based on non-transformed data for fibre diameter (Table 3.4) indicate that the intercept as well as the regression coefficient (slope) did not differ from zero and one, respectively.

Comparing individual data that depicts the regressions of sire breeding values based on transformed fibre diameter data on breeding values based on non-transformed data for the sires originating from the High and Low flocks, both the slopes and intercepts differed according to classification (Table 3.7). However, the differences between the High and Low groups were much less evident than that of body weight and clean fleece weight. The data of the High group was characterised by an intercept below zero and a slope below one. The Low group showed exact opposite of the High group and revealed an intercept above zero and a slope above one. A scatter-plot depicting these relationships of the High and Low groups is provided in Figure 3.6. The information in Table 3.7 and Figure 3.6 suggests that sire breeding values of those sires originating from flocks in low environments will be adjusted slightly upwards by the transformation while the breeding values for sires from the High flocks will be adjusted downwards. In theory, the effect of these adjustments would be much less obvious than for the other traits.

Table 3.7 Regression equations (SE in brackets) of transformed breeding values on non-transformed breeding values for sires classified as originating from the High and Low flocks for fibre diameter

Classification	Intercept (a) with SE	Slope (b) with SE	Residual Mean Square	R^2	Number of observations
High	-0.064	0.935	0.029	0.901	146
	(0.016)	(0.026)			
Low	0.034	1.045	0.010	0.973	180
	(0.008)	(0.013)			

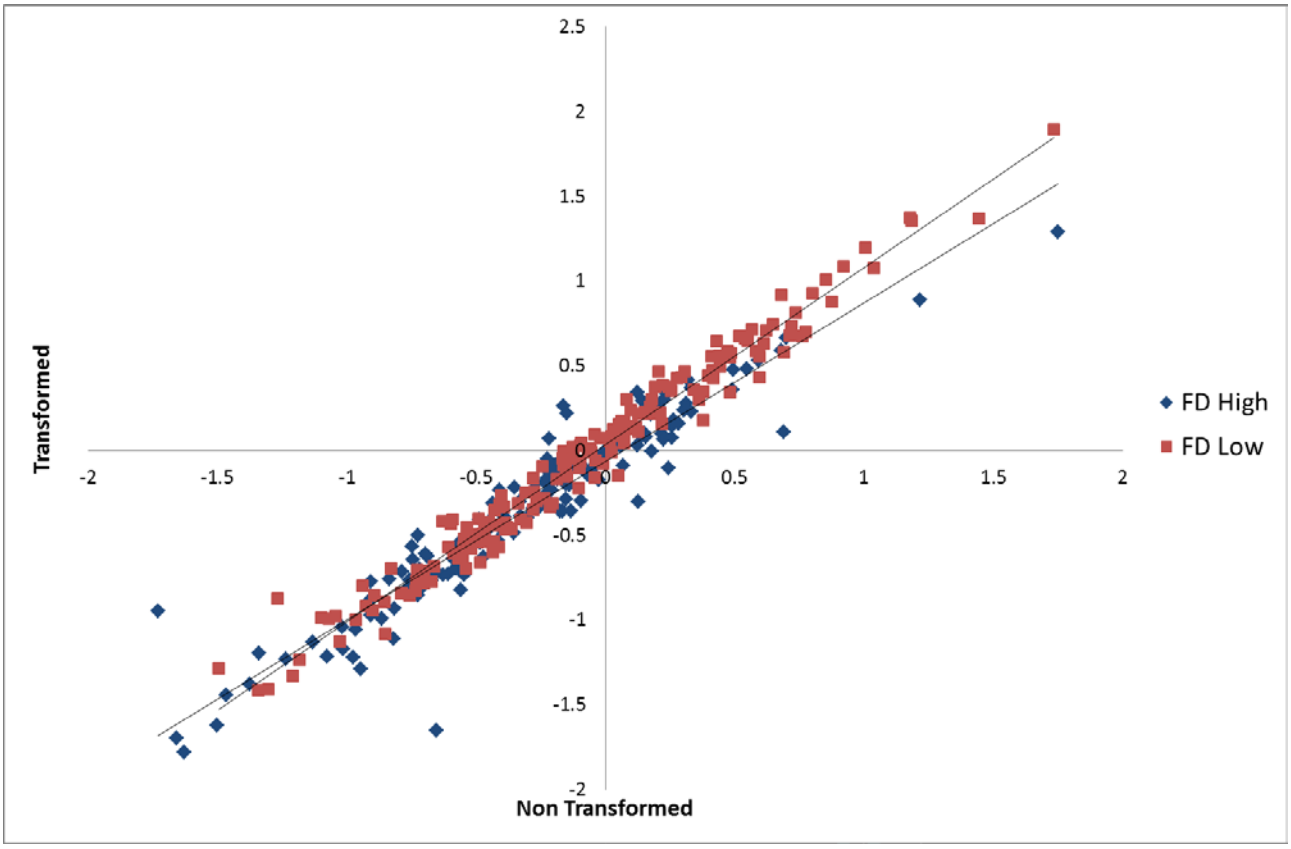

Figure 3.6 Scatter-plots depicting the regressions of sire breeding values based on transformed data on those breeding values based on non-transformed data for fibre diameter in sires originating from high or low environments

3.3.4 Genetic trends

Laas (1982) stated that body weight, clean fleece weight and fibre diameter are regarded as the most important production traits that need to be considered during the selection of the Dohne Merino. Genetic trends for these traits, as well as the transformation applied to the data (transformed vs. non-transformed), and the designated phenotypic groups (High vs. Low) are summarised in Table 3.8. The realised genetic

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improvement in body weight for the High group (0.327 kg per annum) was considerably higher than in the Low groups (0.219 kg per annum) when non-transformed data were considered, respectively, representing 0.54 and 0.55% of overall phenotypic means of the designated groups. This difference in genetic gain was substantially reduced when the results of the transformed data were considered, yielding corresponding regressions of 0.323 kg per annum (0.53% of overall phenotypic mean) and 0.271 kg per annum (0.68% of overall phenotypic mean), respectively. Although the intercepts also differed according to the designation of the flocks, this difference was accordingly reduced when transformed data were used. It was thus clear that overall genetic change in the High and Low groups was rendered much more comparable when transformed data were considered, as was also apparent from Figures 3.7(a) and 3.7(b).

The effect of transforming the data was even more evident for the High and Low groups when clean fleece weight was analysed. The annual genetic change in the High and the Low groups were comparable when non-transformed data were used (0.009 vs. 0.011 kg per annum and also amounting to 0.23 and 0.49% of overall phenotypic means, respectively). However, the genetic trend in the High group was on a higher genetic level during the period the records used in this study were recorded, as indicated by a significant difference between the intercepts of the respective graphs (-17.4 kg vs. -22.1 kg, respectively). Transforming the data appropriately resulted in the genetic trends being more comparable for the range of years with records (Figure 3.8a and 3.8b), although an appreciable difference persisted as far as the intercepts were concerned. The genetic trend in the High group was actually slightly below that of the Low group in absolute terms when the output from the transformed data was considered (0.005 vs. 0.007 kg per annum respectively). In this case, the genetic trends amounted to 0.13 and 0.33% of the respective overall phenotypic means, respectively. Therefore, the transformation of data had a profound effect on the derived genetic trends for clean fleece weight (Table 3.8 and Figure 3.8a and 3.8b).

In contrast to the genetic trends for body weight and clean fleece weight, the effect of the transformation was substantially less for fibre diameter. All the derived genetic trends ranged between -0.055 (-0.30% of overall phenotypic mean) and -0.072 μm per annum (-0.37% of overall phenotypic mean) across categories involving the designation of the flocks (High vs. Low), and the treatment of the data (transformed vs. non-transformed). Genetic change in the Low group was consistently slower than in the High group, irrespective of transformed or non-transformed data being used (Figure 3.9a and 3.9b).

Progress in body weight and fibre diameter in the current study was generally faster than in the study of Cloete *et al*. (1998) on the Dohne Merino stud maintained at the Kromme Rhee Research Farm. Genetic change in body weight in the present study ranged from 0.21 to 0.33 kg per annum compared to a value of 0.15 kg in the study by Cloete *et al*. (1998). Corresponding values for fibre diameter amounted to between -0.055 and -0.072 μm in the present study, which are higher than the value of -0.011 μm observed by Cloete *et al*. (1998). Greater genetic change (0.016 kg per annum) in clean fleece weight was reported by Cloete *et al*. (1998). It is notable that both studies reported genetic change in the desired directions,

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confirming that the objective of the Dohne Merino breeders are to increase body weight and clean fleece weight, while fibre diameter is being reduced.

Table 3.8 Genetic change per annum (b-value) and intercepts (a-value) with SE in brackets as well as corresponding correlation coefficients (r-value) of transformed and non-transformed data for the traits analysed

	Non-transformed		**Transformed**	
Trait	High-group	Low-group	High-group	Low-group
Body weight (kg)	b =0.3272	b = 0.2191	b = 0.3226	b = 0.2708
	(0.0197)	(0.0086)	(0.0159)	(0.0109)
	a = -655.37	a = -440	a = -646.41	a = -543.47
	(39.4601)	(17.2412)	(31.8502)	(21.7665)
	r = 0.974	r = 0.989	r = 0.982	r = 0.988
Clean fleece weight (kg)	b = 0.0087	b = 0.011	b = 0.0049	b = 0.0074
	(0.0008)	(0.0008)	(0.0008)	(0.0006)
	a = -17.35	a = -22.12	a = -9.8069	a = -14.84
	(1.6855)	(1.6818)	(1.5363)	(1.1375)
	r = 0.936	r = 0.959	r = 0.855	r = 0.959
Fibre diameter (micron)	b = -0.0724	b = -0.0546	b = -0.0686	b = -0.0576
	(0.0035)	(0.0029)	(0.0032)	(0.0034)
	a = 145.29	a = 109.69	a = 137.54	a = 115.72
	(7.0357)	(5.8764)	(6.4163)	(6.8318)
	r = -0.983	r = -0.979	r = -0.984	r = -0.975

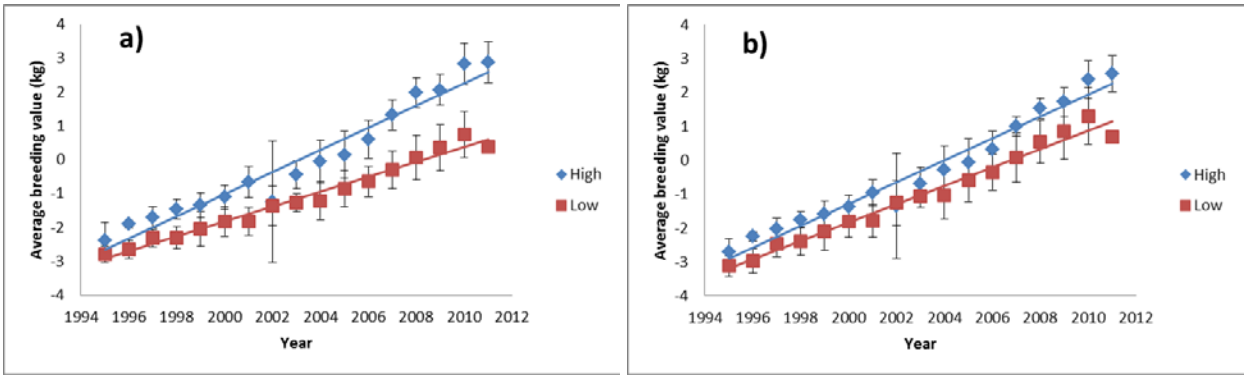

Figure 3.7 Genetic trends for body weight in the High and Low groups using non-transformed data (a), and transformed data (b)

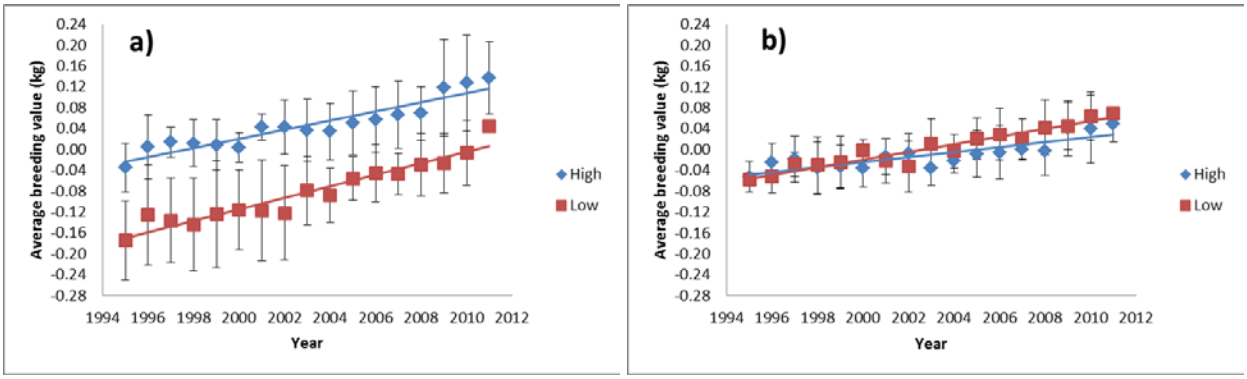

Figure 3.8 Genetic trends for clean fleece weight in the High and Low groups using non-transformed data (a), and transformed data (b)

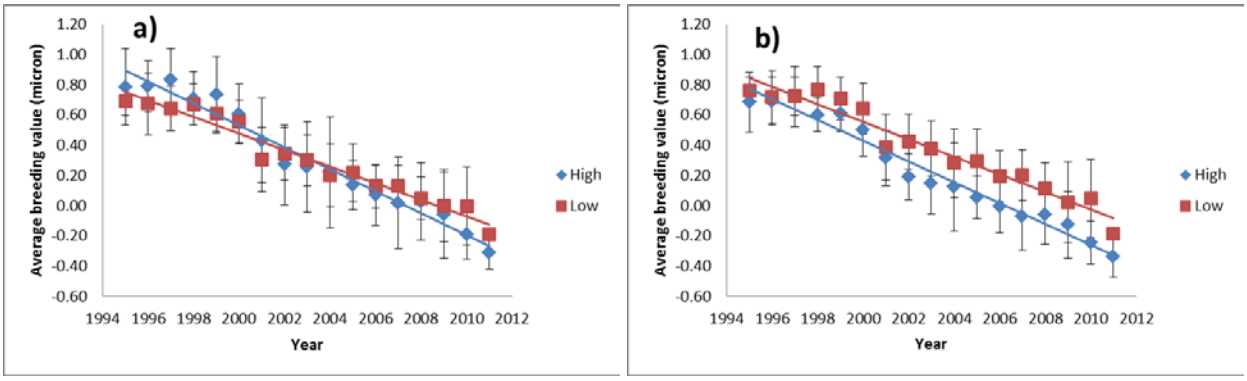

Figure 3.9 Genetic trends for fibre diameter in the High and Low groups using non-transformed data (a), and transformed data (b)

3.4 Conclusions

Generally, the three traits under consideration were moderately heritable, indicating the existence of substantial genetic variation in these traits; hence genetic gains should accrue when purposeful selection is

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applied according to a specific objective. This was also demonstrated very clearly by the derived genetic trends, showing substantial improvements in body weight and clean fleece weight, while fibre diameter was reduced. There were some unfavourable genetic correlations (i.e. fibre diameter with body weight and clean fleece weight). However, the magnitude of these correlations (<0.20) suggest that less unfavourable responses may be expected if selection is targeted at one trait. In addition, all these traits should be considered or included in genetic selection programs. The interaction of sires with contemporary groups, as an indication of the genotype by environment interaction, was relatively small and constituted approximately 2% of the overall phenotypic variance for all three traits. It follows that large-scale re-ranking of sires is unlikely, unless for mediocre sires.

It was evident that the transformation of data to percentages resulted in breeding values for sires that originated from flocks maintained in limiting environments (Low group) being adjusted upwards. In contrast, the breeding values of sires originating from flocks where the environment did not limit production (High group) were adjusted downwards. These effects were markedly obvious for the quantitative traits body weight and clean fleece weight, but present to a much lesser extent for fibre diameter. The transformation thus had a profound effect on genetic trends for those flocks designated as member of the High and Low groups in the case of the former two traits (body weight and clean fleece weight). In contrast, fibre diameter was affected to a much lesser extent by the transformation of the data, which could be due to the comparatively low coefficient of variation obtained in early analysis. The transformation of body weight and clean fleece weight data (as described in this chapter) is thus recommended.

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Chapter 4

The effect of using phantom groups on the accuracy of breeding values for animals upgraded from commercial herds to stud breeders in Dohne Merinos

W. Jordaan[1], S.W.P. Cloete[1,2], J.J. Olivier[2] and K. Dzama[1]

[1] *Department of Animal Sciences, University of Stellenbosch, Matieland, 7600*

[2] *Department of Animal Production, Elsenburg, 7607*

Abstract

Animals entering the national recorded Dohne Merino flock from a commercial flocks lack pedigree information, which may lead to underestimated breeding values for progeny of such individuals. All animals originating from a cross between F3 ewes and a Dohne Merino stud ram, with unknown parents were assigned to phantom parent groups according to one of the four pathways of selection while also including the year the animal first progeny was born as part of the classification. Such animals were treated in three different ways, namely: no specific treatment was applied (non-phantom), or classified according to phantom groups with a maximum of 100 parents (100 phantom) or as phantom groups with a maximum of 500 parents (500 phantom). Average breeding values in each year (1992 – 2011) were calculated for each of the two groups, namely the progeny (F4) of the F3 ewes mated to a top-stud Dohne Merino stud ram compared to all other pedigreed animals, termed as RES in the F5 and subsequent generations. Traits that were considered involved body weight, clean fleece weight and fibre diameter. The inclusion of phantom parent groups rendered genetic trends in F4 animals comparable to that of the full pedigreed portion of animals in the analyses. Derived genetic trends revealed that body weight and fibre diameter responded significantly faster in absolute terms in the full pedigreed animals (0.231 kg and -0.056 μm vs. 0.214kg and -0.052 μm per annum, respectively). Clean fleece weight showed slightly faster genetic improvement in the F4 grouping in the analysis than in the pedigreed part of the population (0.0047 kg vs. 0.0039 kg for pedigreed animals). It is recommended that phantom parents should be routinely included in the genetic analyses involving the National Dohne Merino flock due to the greater probability of progeny being upgraded from ewes originating from a commercial base population to be selected in the recorded population.

Keywords: Phantom groups, genetic trends, estimated breeding values

4.1 Introduction

The Dohne Merino Breeding Association makes use of an open nucleus system to facilitate flow of breeding material from commercial flocks to fully recorded studs. The system is developed with the aim to identify young commercial ewes (F3) with favourable production characteristics to be included into the stud in order to broaden the genetic base and to tap on the greater genetic variation in commercial flocks. It is argued that such ewes can strengthen the ram breeding flock by the introgression of favourable alleles for robustness and fitness. Such a system is alleged to ensure that a stud being managed in this way will have high levels of production while also excelling for fitness and robustness.

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The Dohne Merino Manual (2009) states that only the top 20% of the F3 ewes (Progeny of F2 ewes x approved AA Dohne Merino rams) will be approved to move into the stud foundation register if they meet the following criteria: visually meet the breeding standards set by the Dohne Merino Breeder's Society and by conforming to objective selection for body weight and fleece weight.

However, progeny of animals entering the breeding flock from a commercial base (F3 animals) lack depth in pedigree information. The lack of pedigree information resulted that estimated breeding values of these animals are reverted back to the base population, and are often underestimated. The probability of selecting progeny of such animals is thus reduced, with the implication that the advantages are often not realised in the bigger population. The problem of animals entering the recorded population from the commercial industry and thus becoming base parents is not uncommon in livestock breeding, especially in the dairy industry. Such animals are often allocated to specified groups according to the information that is available for them, for instance, base animals with more recent birth years are commonly considered to be on a higher genetic level than those base animals with more distant birth years. Groups constructed in this way during genetic evaluation are commonly referred to as phantom groups (Theron *et al*., 2002; Fikse, 2009). The allocation of base animals to phantom groups allows some control over the different genetic levels that may be present in the broader population termed as the base animals (Westall *et al*., 1988).

The allocation of animals to different phantom groups may be approached in different ways. An approach that is commonly used is to asign the unknown parent to a phantom group corresponding to the year of birth of the animal and according to the sex of the parents of that animal as well as the offspring. This approach results in one of the four pathways of selection (of which each pathway differs in the presumed genetic merit of the parent animals), namely; Sire of Sire (SS), Sire of Dam (SD), Dam of Sire (DS) and Dam of Dam (DD) as described by Schaeffer (2006). Selection intensity differences between animals allocated according to these pathways contribute to the unequal levels of genetic merit in base animals. According to Westall *et al*. (1988), sires have been subjected to appreciably higher selection intensity than dams. It is therefore necessary to accommodate the selection intensity when constructing phantom groups.

The aim of this study was therefore to investigate the effect of inclusion of phantom group classification for animals entering the National Dohne Merino breeding flock from the commercial industry.

4.2 Material and Methods

4.2.1 Data

Performance records information for this study was obtained from the National Small Stock Improvement Scheme database as well as from pedigree l recorded data from the Dohne Merino Breed Society of South

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Africa for animals born from 1992 to 2011. The original data set consisted of 347 581 records and included animals with records for body weight, clean fleece weight and fibre diameter.

Contemporary groups for the production traits were created from the concatenation of flock-year-season-sex-management group (FYSSM). The year and season in the contemporary groups refer to the birth of the animal. The data were transformed according to the method described by Brown *et al*. (2005), where the traits were expressed as a proportion of their contemporary group (CG) means to account for heterogeneous contemporary group means. The outcome of the treatment of the data according to this transformation is described in Chapter 3.

All animals in the F3-generation with unknown parentage were assigned to a phantom group corresponding to the year of birth of their first progeny and to the sex of the unknown parent as well as the animal under consideration. Thus the animal was allocated to one of the four pathways of selection as described by Schaeffer (2006).

Data were analysed to obtain individual breeding values and genetic trends for animals upgraded from the commercial populations with no phantom group classification or with phantom groups (groupings of a maximum of 100 or 500 comparable animals where appropriate). These animals (F4) were compared with those with complete pedigree information and forming part of the F5+-generations.

4.2.2 Statistical analyses

The statistical analyses were divided into sequential steps. Firstly, all animal records in the F3-generation with incomplete parentage (i.e. no sire and/or dam) were assigned to a phantom group. These phantom groups were constructed according to one of the four pathways indicative of the genetic merit of an animal, as well as the year of birth of the animal.

Using ASReml, the number of animals in each phantom group was estimated. The phantom parents were grouped per year and divided into smaller groups involving maxima of either 100 animals per group (100 phantom grouping) or 500 animals per group (500 Phantom grouping) of which the total number of groups in every grouping for each year can be seen in Table 4.1 and Table 4.2, respectively. These groupings were researched as it was postulated that information contained therein is likely to assist with the accurate genetic appraisal of the F4 generation in particular, in comparison with the fully pedigreed animals in the analysis (F5+ generations), termed as the RES generation subsequently.

A multi-trait analysis model was developed where estimates of the fixed effects, additive genetic values and other random components were calculated as described in Chapter 3. The ASReml programme (Gilmour *et al*., 2009) was used for this purpose. Animal solutions emanating from the multi-trait analysis were used as predicted breeding values for the animals. The genotype by environment interaction was modelled by the inclusion of the sire-flock-season (SFS) interaction as an additional random factor. Phantom parent groups

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were also fitted as a random factor. Fixed effects for this model were estimated with SAS Enterprise Guide program (SAS, 2007) in a general linear model (GLM) to assess the effect of each main effect on each of the three traits being analysed, as described in Chapter 3. Dam age and age of the animal at recording were used as covariates in the model. The fixed effects and covariates that were included in the model and were accounted for as sources of variation were the following:

Age Age at performance measurement. This effect was plotted as a polynomial, thus only the slope and no intercept, and can also be defined as a term with two columns having centred and scaled linear coefficients in the first column and centred and scaled quadratic coefficients in the second column (ASReml User Guide, Gilmour *et al*., 2009).

AgeDam The age of the dam, ranging from one to ten years of age and was plotted as a linear regression

BStat The rearing type of the animal, involving singles, twins or triplets.

CG The contemporary group which was defined by flock-year-season-sex-management group (FYSSM).

The following three-trait model was decided upon (in matrix notation):

$$\mathbf{y = Xb + Z_1a + Z_2sfs + Z_3pg + e}$$

where **y** is a vector of observations for body weight , clean fleece weight and fibre diameter

b is a vector describing all the fixed effects in the model

a is a vector of direct additive genetics

sfs is a vector of sire x flock x season interaction effects

pg is a vector of phantom parents

X, Z_1, Z_2, Z_3 is incidence matrices relating data to the above vectors

e is a vector of random residuals

The final data set that comprised of 296 941, 287 928 and 288 127 records for body weight, clean fleece weight and fibre diameter, respectively, was used to derive genetic trends. Average breeding values, for each trait, were calculated for the F4-generation (without complete pedigree information) as well as for the RES generation for models involving no phantom groups, as well as for phantom groups involving maxima of either 100 or 500 individuals. Average breeding values were calculated using standard database software (Microsoft Access) as well as SAS Enterprise Guide (SAS, 2007) for each trait within the three different groupings specified previously (non-phantom, 100 phantom and 500 phantom). Genetic trends were plotted for those animals entering the flock from a commercial background and fully pedigreed portion of the population (F4 and RES generations respectively) and plotted to depict the genetic trends. Averaged breeding values within years were accompanied by their standard errors for the three different groups specified above. These breeding values were regressed on birth years to depict the observed genetic trends for each option.

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4.3 Results and Discussion

Data revealed that there were 88 758 animals in the F3 generation with no or incomplete parentage, i.e. where either the sire or the dam or both were not recorded. Each of these individuals was assigned to a phantom parent according to the pathways described above and the year of birth of the animal. Flock of origin was not included in this classification, because it would have resulted in very small phantom groups. These phantom parents were counted by their number of appearance using ASReml, ranging from the years of 1994 to 2010, and were then grouped.

By comparing Table 4.1 and Table 4.2 it is evident that the 500 phantom grouping was more stringent than the 100 phantom grouping when looking at the phantom parents' number of appearances. Due to the lack of pedigree information of the dam the appearance of phantom parents also seems primarily from the Dams pathway of selection (DD and SD) in both groupings (both the 100 and 500 Phantom grouping). It is highly probable that this is a reflection of the upgrading system for the Dohne Merino breed from the commercial base population, as is described under heading 2.3 in Chapter 2.

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Table 4.1 Table depicting the number of phantom parent groups based on maxima of 100 phantom parents over the time period from 1994 to 2010

			100 Phantom	
Year	**SS**	**DS**	**DD**	**SD**
1994	1023	1023	19123	19123
1995	145	145	1965	1965
1996	-	-	2089	2089
1997	144	144	2435	2435
1998	-	-	2168	2168
1999	164	164	1604	1604
2000	-	-	1985	1985
2001	-	-	1820	1820
2002	-	-	1399	1399
2003	-	-	1352	1352
2004	-	-	1377	1377
2005	-	-	1594	1594
2006	-	-	1446	1446
2007	-	-	1327	1327
2008	-	-	807	807
2009	-	-	249	249
2010	-	-	163	163

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Table 4.2 Table depicting the number of phantom groups based on maxima of 500 phantom parents over the time period from 1994 to 2010

		500 Phantom		
Year	**SS**	**DS**	**DD**	**SD**
1994	1473	1473	19123	19123
1995	-	-	1965	1965
1996	-	-	2089	2089
1997	-	-	2435	2435
1998	-	-	2168	2168
1999	-	-	1604	1604
2000	-	-	1985	1985
2001	-	-	1820	1820
2002	-	-	1399	1399
2003	-	-	1352	1352
2004	-	-	1377	1377
2005	-	-	1594	1594
2006	-	-	1446	1446
2007	-	-	1327	1327
2008	-	-	1219	1219
2009	-	-	-	-
2010	-	-	-	-

Genetic trends for F4 animals and pedigreed animals (RES) involving the three traits according to the three analyses excluding phantom groups (non-phantom) and incorporating maxima of 100 and 500 phantom parents (100 phantom and 500 phantom respectively) are summarised in Table 4.3. Schaeffer (2006) stated that each pathway reflects a different intensity of selection on the offspring. However, solutions that reflect differences in the genetic merit of parents transferred to animals with unknown parentage are often not very smooth over time and they do not necessarily follow the expected genetic trend in the population. These solutions could reflect genetic trends if the animals with unknown parentage are a random sample of all contemporary animals (sires or dams that were present during a certain time period) and also that year groupings will result in estimated trends being an average. Theron *et al*. (2002) found that the inclusion of phantom parent groups in the model had a minor influence on the estimation of (co)variance components, but had a substantial effect on the estimated genetic trends for SA Holstein cattle. Genetic trends for both the daughters of local sires of the daughters of imported sires benefited from the inclusion of phantom parent groups in the analyses of the latter authors.

The inclusion of phantom groups also had a profound effect on the genetic merit (as indicated by derived EBV's) of the part of the population (F4's) entering the analysis from the commercial industry in the present study (Table 4.3). The regression coefficient depicting genetic change approximately doubled for body

weight and fibre diameter, while a four-fold increase was observed for clean fleece weight. The number of phantom parents grouped together (100 or 500) did not seem to exert a marked influence on the outcomes of the analyses involving genetic trends. The inclusion of phantom groups had a lesser influence on the pedigreed part of the population, but the slopes and intercepts of the RES group were still slightly lower in the analyses excluding phantom groups than in the analyses that included phantom groups. The inclusion of phantom groups rendered genetic trends in the F4-population roughly comparable to that observed in the pedigreed part of the population. Plotted genetic trends for the respective traits will now be discussed per trait.

Table 4.3 Genetic improvement per annum (b-value) and intercepts (a-value) with SE in brackets as well as corresponding correlation coefficients (r-value) of the F4-generation as well as the RES (fully pedigreed animals) for body weight, clean fleece weight and fibre diameter according to the three different analyses conducted (non-phantom, 100 phantom and 500 phantom)

Trait	Non Phantom		100 Phantom		500 Phantom	
	F4	**RES**	**F4**	**RES**	**F4**	**RES**
Body weight	b = 0.1077	b = 0.1645	b = 0.2144	b = 0.2305	b = 0.2066	b = 0.2218
	(0.0078)	(0.0107)	(0.0090)	(0.0097)	(0.0103)	(0.0102)
	a = -216.28	a = -329.57	a = -430.06	a = -462.04	a = -414.39	a = -444.66
	(15.6968)	(21.4837)	(18.0596)	(19.4152)	(20.5814)	(20.4904)
	r = 0.955	r = 0.964	r = 0.984	r = 0.984	r = 0.978	r = 0.981
Clean fleece weight	b = 0.0011	b = 0.0022	b = 0.0047	b = 0.0039	b = 0.0047	b = 0.0040
	(0.0004)	(0.0004)	(0.0004)	(0.0005)	(0.0004)	(0.0005)
	a = -2.30	a = -4.47	a = -9.42	a = -7.83	a = -9.37	a = -8.02
	(0.8111)	(0.8795)	(0.8743)	(0.9382)	(0.8098)	(0.9417)
	r = 0.554	r = 0.768	r = 0.930	r = 0.891	r = 0.939	r = 0.895
Fibre diameter	b = -0.0286	b = -0.0422	b = -0.0519	b = -0.0560	b = -0.0501	b = -0.0541
	(0.0017)	(0.0023)	(0.0021)	(0.0025)	(0.0021)	(0.0026)
	a = 57.54	a = 84.70	a = 104.32	a = 112.44	a = 100.59	a = 108.65
	(3.4077)	(4.6611)	(4.1311)	(5.0944)	(4.1705)	(5.2418)
	r = 0.970	r = 0.974	r = 0.986	r = 0.982	r = 0.985	r = 0.980

4.3.1 Body weight

Table 4.4 Table depicting 95% confidence intervals of body weight, clean fleece weight and fibre diameter breeding values for the three different groupings (non-phantom, 100 phantom and 500 phantom) of the F4-generation as well as RES (fully pedigreed) generation over the time period of 20 years (1992 – 2011)

F4 generation									
Trait	**Body weight**			**Clean fleece weight**			**Fibre diameter**		
	Non-Phantom	**100 Phantom**	**500 Phantom**	**Non-Phantom**	**100 Phantom**	**500 Phantom**	**Non-Phantom**	**100 Phantom**	**500 Phantom**
95% interval (slope)	0.09 – 0.12[a]	0.20 – 0.23[a]	0.19 – 0.23	0.0003 – 0.0020[a]	0.0038 – 0.0056[a]	0.0038 – 0.0055	-0.03 – -0.03[a]	-0.06 – -0.05[a]	-0.06 – -0.05
95% interval (intercept)	-249.26 – -183.31	-468.00 – -392.12	-457.63 – -371.15	-4.00 – -0.60	-11.26 – -7.85	-11.07 – -7.67	50.38 – 64.70	95.64 – 113.00	91.83 – 109.35
RES generation									
Trait	**Body weight**			**Clean fleece weight**			**Fibre diameter**		
	Non-Phantom	**100 Phantom**	**500 Phantom**	**Non-Phantom**	**100 Phantom**	**500 Phantom**	**Non-Phantom**	**100 Phantom**	**500 Phantom**
95% interval (slope)	0.14 – 0.19[b]	0.21 – 0.25[b]	0.20 – 0.24	0.0013 – 0.0032[b]	0.0029 – 0.0049[b]	0.0030 – 0.0050	-0.05 – -0.04[b]	-0.06 – -0.05[b]	-0.06 – -0.05
95% interval (intercept)	-374.70 – -284.43	-502.83 – -421.25	-487.71 – -401.62	-6.32 – -2.62	-9.80 – -5.85	-10.00 – -6.05	74.91 – 94.50	101.74 – 123.15	97.63 – 119.66

[a] *Slopes differ significantly in F4 generation between non-phantom groupings and 100 phantom parent grouping for bodyweight, clean fleece weight and fibre diameter*

[b] *Slopes differ significantly in RES generation between non-phantom groupings and 100 phantom parent grouping for bodyweight, clean fleece weight and fibre diameter*

Genetic change in body weight (as depicted by the regression coefficients of average annual breeding values on birth year in Table 4.3) for the F4-generation was significantly lower ($P<0.05$) when compared to the RES grouping in the analysis without phantom groups (Figure 4.1a), namely 0.1077 kg per annum and 0.1645 kg per annum, respectively. The genetic trends became much more comparable in the analyses involving phantom groups, as depicted in Figure 4.1b for phantom groups based on the 100 phantom parents grouping. Although the absolute regression coefficients regarding the analyses involving phantom

groups still favoured the RES population above the F4-population, no statistically significant difference could be demonstrated between the respective genetic trends. Genetic trends (for body weight, clean fleece weight and fibre diameter) involving 500 phantom parents grouped together were largely similar to that based on groupings of 100 phantom parents, and are therefore not shown in graphs.

In Table 4.4 it is evident that the inclusion of phantom groups rendered genetic trends in F4 animals without pedigree information comparable to that of the pedigreed portion of animals in the analyses by relating the 95% confidence intervals of the slope and intercept (Table 4.4). This result is similar to that described by Theron *et al*. (2002) for South African Holstein cattle.

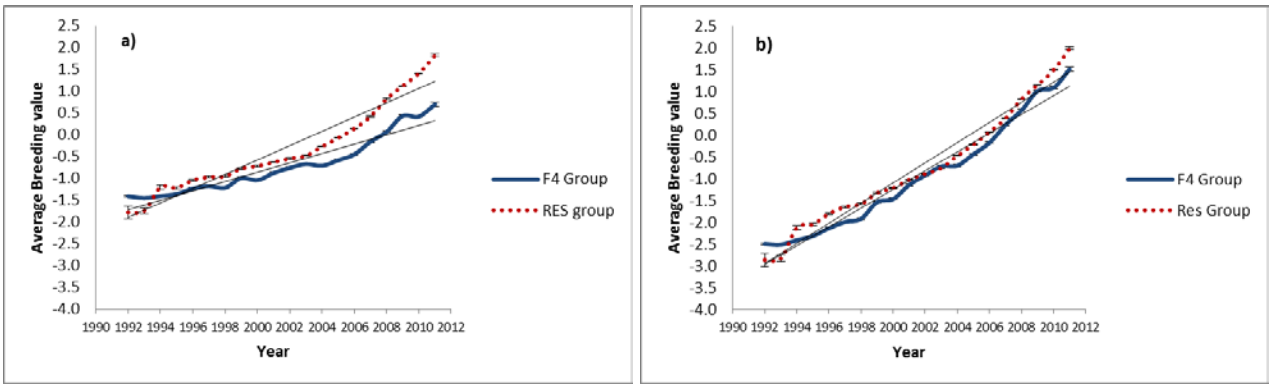

Figure 4.1 Genetic trends for body weight in the F4 and F5+ generation (RES) using non-phantom (a) and the 100 phantom (b) groupings

In Figure 4.1 (a and b), the standard errors applicable to annual means for the average breeding values are depicted for both The F4 and RES generations. However, these error bars are so small they are hardly discernible on the graph. The exception of the previous statement is that the standard errors obtained in the years from 1992 to1994 in the RES generation for both analyses depicted in Figure 4.1 are obviously higher. The same trend is evident in 2011 for the F4 generation. This result could obviously be attributed to the lower numbers for pedigreed animals at the beginning of the recorded era in the early 1990's, while the remaining number of F4-animals without pedigrees are obviously very few in 2011.

Swanepoel (2006) obtained a genetic improvement of 0.1542 kg per annum over the time period of 1992 to 2003 for body weight in a study he did with Dohne Merinos, which was similar to the value obtained in this study for the RES generation in the non-phantom analysis. Studies on the Western Cape Dohne Merino nucleus flock over the period of 1980 to 1994 revealed a genetic change of 0.145 kg per annum for yearling live weight (Cloete *et al*., 1998). In contrast, De Klerk (1990) supplied evidence of a study on the Dohne Research Institute Dohne Merino flock wherein the genetic change for 18-month live weight amounted to only 0.059 kg per annum, which was much slower progress than that recorded in the current study.

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4.3.2 Clean fleece weight

Regression coefficients for average annual breeding values for clean fleece weight on birth year (Table 4.3) show that genetic improvement in the non-phantom grouping was significantly higher in the RES generation than in the F4 generation (0.0022 and 0.0011, respectively). This difference is also evident in Figure 4.2a. The genetic trends became much more comparable in the analyses involving phantom groups, as depicted in Figure 4.2b for phantom groups based on 100 phantom parents. The absolute regression coefficients in this case favour the F4 population and not the RES population, in contrast to the results found for bodyweight. Genetic trends involving the analysis in the 500 phantom grouping are not shown in a graph due to the fact that it was largely similar to the 100 phantom grouping.

In Table 4.4, it is evident that the inclusion of phantom groups rendered genetic trends in F4 animals without pedigree information more comparable to that of the pedigreed portion of animals in the analyses when considering the 95% confidence intervals of the slope and intercept.

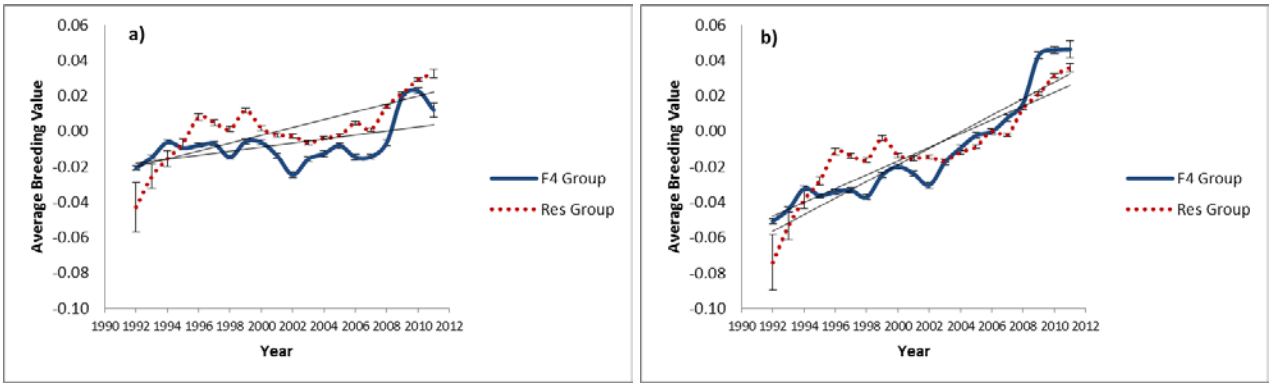

Figure 4.2 Genetic trends for clean fleece weight in the F4 and F5+ generation (RES) using the non-phantom (a) and 100 phantom (b) groupings

The standard errors depicted in Figure 4.2 (a and b) of the average breeding values for both generations are all small. The exception is once again that the standard errors obtained in the early years for the RES generation are appreciably higher than in the F4 generation, as for body weight. The same applies for the year 2011 in the F4 generation, as was also observed for body weight.

A similar value of 0.0035 kg per annum was recorded as genetic change for clean fleece weight by Swanepoel (2006) in a study conducted on Dohne Merinos between 1992 and 2003, while Cloete *et al*. (1998) recorded a higher genetic change of 0.016 kg per annum in the Western Cape Dohne Merino nucleus flock. Although the genetic change of 1 – 2% per annum is commendable, and >0.5% is acceptable, the current genetic change is in the right direction.

4.3.3 Fibre diameter

The goal of selection for finer wool can be achieved by obtaining a negative slope for fibre diameter. In the analyses without phantom groups (Table 4.3) the RES generation showed a significantly superior genetic improvement (-0.0422 µm per annum) than the F4 generation (-0.0286 micron per annum) as depicted in Figure 4.3a. In the analyses involving the 100 phantom parents grouping, the genetic trends became more comparable (as depicted in Figure 4.3b). Similar to the trends observed in bodyweight, the absolute regression coefficients still favoured the RES population above the F4 population. However, no conclusive statistically significant difference (P > 0.05) could be demonstrated between the observed genetic trends (regarding slope coefficients) between the F4 and RES generation regarding the 100 phantom parent grouping (Table 4.4).

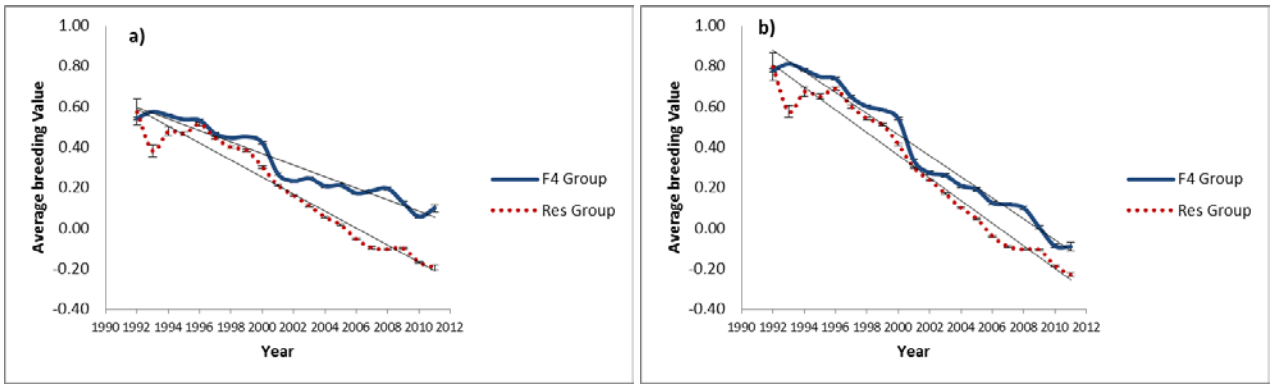

Figure 4.3 Genetic trends for fibre diameter in the F4 and F5+ generation (RES) using non phantom (a) and 100 phantom (b) groupings

Standard errors for the RES generation were once again larger in magnitude in the early days of recording (Figure 4.3a and 4.3b), while those for the F4 generation were inflated in 2011. This trend was also evident in the graphs for body weight (Figure 4.1) and clean fleece weight (Figure 4.2), and is attributed to the relative numbers of RES and F4 numbers, as was indicated earlier.

Swanepoel (2006) observed a genetic change of -0.039 micron per annum for fibre diameter in the Dohne Merino over the time period from 1992 to 2003. The value in the latter study corresponds well with the genetic change obtained in the current study in the RES generation without including phantom groups. Cloete *et al*. (1998) obtained an appreciably slower genetic change of -0.011 micron per annum in the Western Cape Dohne Merino nucleus flock, which reflected a less favourable genetic change considering that selection in the Dohne Merino is favouring the production of finer wool.

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4.4 Conclusions

This study revealed that genetic trends of progeny of animals entering the national Dohne Merino flock with unknown parentage (the F4 generation) and animals entering the flock with known parentage (RES generation) differed significantly when derived from analyses with and without phantom parent groups. Genetic change in the RES population, in general, was appreciably faster than in the F4 population when based on analyses without phantom groups. However, it was evident that the inclusion of phantom parent groups in the analyses involving all traits rendered the F4 generation more comparable to the pedigreed portion of the population. A similar trend was observed in South African Holstein dairy cattle in literature that was cited. It is therefore recommended that phantom parents should be routinely included in genetic analyses involving the National Dohne Merino flock.

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Chapter 5

General conclusions and recommendations

5.1 Conclusions

Heritability estimates for the traits were generally moderate for the quantitative production traits (body weight and clean fleece weight), and high (>0.40) for fibre diameter, a qualitative trait. Body weight had a heritability of 0.265 and 0.210 for clean fleece weight, both which was well within the range of other published estimates. Fibre diameter had a heritability estimate of 0.437 which was lower than other published estimates on predominantly Merinos, but consistent with previous estimates on Dohne Merinos. Genetic correlations were unfavourable at below 0.20 for body weight and clean fleece weight with fibre diameter (0.139 and 0.169 respectively). The levels of heritability of the traits indicate genetic variation that is present, which may suggest that these traits should respond well to directed and purposeful selection. This contention was well supported by genetic trends that were also reported in the thesis.

The transformation of the data to proportions of contemporary group means resulted in substantially reduced coefficients of variation for body weight and clean fleece weight. This may indicate less phenotypic variation and also decreases the scope of selection for these traits. However, the magnitude of genetic trends was not markedly affected. Moreover, it was evident that the transformation of the data assisted in accounting for the effects of the diverse production environments. This effect of transforming the data, as judged by the coefficient of variation, was more evident in the quantitative traits body weight and clean fleece weight and not so obvious in the quality trait, fibre diameter. When flocks were allocated to high, medium and low groups based on phenotypic performance, data transformation caused breeding values of sires originating from the low groups being adjusted upwards, while those from the high group were adjusted downwards. The observed adjustments were once again more pronounced for the traits, body weight and clean fleece weight, than in fibre diameter. Genetic trends for high and low flocks based on non-transformed data were quite distinctly different for body weight and clean fleece weight, but the effect of designation according to phenotypic production (high or low) was substantially reduced in genetic trends based on transformed data. It was thus concluded that the transformation of data assisted in rendering breeding values estimated for body weight and clean fleece weight in sires from phenotypically divergent flocks more comparable. It was thus surmised that such breeding values are likely to predict offspring performance with a greater degree of accuracy. Genetic trends for fibre diameter were not affected to the same extent, and genetic change in the low group was consistently slower than that in the high group for fibre diameter, irrespective of whether transformed or non-transformed data were used.

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Animals entering the flock with unknown parentage from a commercial base and animals entering the flock with known parentage responded quite differently to analyses with and without phantom parent groups being modelled in the analyses. Genetic trends for fully pedigreed animals derived from analyses where no phantom parents were modelled were appreciably more favourable in the desired direction for all traits than for those animals entering the pedigreed flock from a commercial base with no or limited pedigree information. It was evident that the inclusion of phantom parent groupings in analyses involving all traits rendered the animals with unknown parentage more comparable to the pedigreed portion of the population. The genetic analyses for animals with unknown parentage will result in more accurate and reliable breeding values if phantom parents are modelled in the analysis. Such animals are then more likely to add to the robustness and adaptability of the national flock by producing progeny that may actually be selected, as is envisaged by members of the Dohne Merino Breeder's Society.

5.2 Recommendations

Finally, it is clear that the breed analysis of the Dohne Merino benefitted from the transformation of particularly body weight and clean fleece weight data to account for heterogeneous variances in contemporary group means. Similarly, those animals entering the recorded population from a commercial base, and without pedigree information, were more accurately assessed for their genetic potential when phantom groups were modelled in the analysis. It is thus recommended that the national analysis should be adapted accordingly, so that industry can benefit from more accurate breeding values derived in this way. Moreover, similar advantages may be present in other breeds participating in the National Small Stock Improvement Scheme. Research to verify this and to adapt other breed analyses, if appropriate, should be undertaken.